

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 6, 2001, 16:55:46 ; Search time 39.01 Seconds

(Without alignments)

211.220 Million cell updates/sec

Title: US-08-403-803-2.COPY\_45\_750

Sequence: 706 1 SSNHTVTPHNNKAFIDR.....QIVAAFPVQAAETSEVA 706

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 374700 seqs, 117207915 residues

Word size : 6

Total number of hits satisfying chosen parameters: 2718

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :  
1: sp\_archea:  
2: sp\_bacteria:  
3: sp\_eukarya:  
4: sp\_fungi:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mollusca:  
8: sp\_plant:  
9: sp\_protist:  
10: sp\_reptile:  
11: sp\_rodent:  
12: sp\_urochordate:  
13: sp\_vertebrate:  
14: sp\_unclassified:

Pred. No. is the number of results predicted by chance to have a  
score at least as high as the observed score, assuming random  
and is derived by analysis of the total score distribution.

## SUMMARIES

Mon Apr 9 11:14:16 2001	us-08-403-803-2.copy_45_750.olg.rep	Page 3
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557	6	0.8	257	10	Q9W36	Q9W36	arabidopsis
558	6	0.8	258	10	Q9W37	Q9W37	arabidopsis
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560	6	0.8	260	10	Q9W39	Q9W39	arabidopsis
561	6	0.8	261	10	Q9W40	Q9W40	arabidopsis
562	6	0.8	262	10	Q9W41	Q9W41	arabidopsis
563	6	0.8	263	10	Q9W42	Q9W42	arabidopsis
564	6	0.8	264	10	Q9W43	Q9W43	arabidopsis
565	6	0.8	265	10	Q9W44	Q9W44	arabidopsis
566	6	0.8	266	10	Q9W45	Q9W45	arabidopsis
567	6	0.8	267	10	Q9W46	Q9W46	arabidopsis
568	6	0.8	268	10	Q9W47	Q9W47	arabidopsis
569	6	0.8	269	10	Q9W48	Q9W48	arabidopsis
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571	6	0.8	271	10	Q9W50	Q9W50	arabidopsis
572	6	0.8	272	10	Q9W51	Q9W51	arabidopsis
573	6	0.8	273	10	Q9W52	Q9W52	arabidopsis
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576	6	0.8	276	10	Q9W55	Q9W55	arabidopsis
577	6	0.8	277	10	Q9W56	Q9W56	arabidopsis
578	6	0.8	278	10	Q9W57	Q9W57	arabidopsis
579	6	0.8	279	10	Q9W58	Q9W58	arabidopsis
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581	6	0.8	281	10	Q9W60	Q9W60	arabidopsis
582	6	0.8	282	10	Q9W61	Q9W61	arabidopsis
583	6	0.8	283	10	Q9W62	Q9W62	arabidopsis
584	6	0.8	284	10	Q9W63	Q9W63	arabidopsis
585	6	0.8	285	10	Q9W64	Q9W64	arabidopsis
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601	6	0.8	301	10	Q9W80	Q9W80	arabidopsis
602	6	0.8	302	10	Q9W81	Q9W81	arabidopsis
603	6	0.8	303	10	Q9W82	Q9W82	arabidopsis
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617	6	0.8	317	10	Q9W96	Q9W96	arabidopsis
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624	6	0.8	324	10	Q9W103	Q9W103	arabidopsis
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707	6	0.8	407	10	Q9W186	Q9W186	arabidopsis
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920	6	0.8	319.2	Q45686	G45686 entereococo
921	6	0.8	319.2	Q45686	G45686 entereococo
922	6	0.8	319.2	Q45686	G45686 entereococo
923	6	0.8	319.2	Q45686	G45686 entereococo
924	6	0.8	319.2	Q45686	G45686 entereococo
925	6	0.8	319.2	Q45686	G45686 entereococo
926	6	0.8	319.2	Q45686	G45686 entereococo
927	6	0.8	319.2	Q45686	G45686 entereococo
928	6	0.8	319.2	Q45686	G45686 entereococo
929	6	0.8	319.2	Q45686	G45686 entereococo
930	6	0.8	319.2	Q45686	G45686 entereococo
931	6	0.8	319.2	Q45686	G45686 entereococo
932	6	0.8	319.2	Q45686	G45686 entereococo
933	6	0.8	319.2	Q45686	G45686 entereococo
934	6	0.8	319.2	Q45686	G45686 entereococo
935	6	0.8	319.2	Q45686	G45686 entereococo
936	6	0.8	319.2	Q45686	G45686 entereococo
937	6	0.8	319.2	Q45686	G45686 entereococo
938	6	0.8	319.2	Q45686	G45686 entereococo
939	6	0.8	319.2	Q45686	G45686 entereococo
940	6	0.8	319.2	Q45686	G45686 entereococo
941	6	0.8	319.2	Q45686	G45686 entereococo
942	6	0.8	319.2	Q45686	G45686 entereococo
943	6	0.8	319.2	Q45686	G45686 entereococo
944	6	0.8	319.2	Q45686	G45686 entereococo
945	6	0.8	319.2	Q45686	G45686 entereococo
946	6	0.8	319.2	Q45686	G45686 entereococo
947	6	0.8	319.2	Q45686	G45686 entereococo
948	6	0.8	319.2	Q45686	G45686 entereococo
949	6	0.8	319.2	Q45686	G45686 entereococo
950	6	0.8	319.2	Q45686	G45686 entereococo
951	6	0.8	319.2	Q45686	G45686 entereococo
952	6	0.8	319.2	Q45686	G45686 entereococo
953	6	0.8	319.2	Q45686	G45686 entereococo
954	6	0.8	319.2	Q45686	G45686 entereococo
955	6	0.8	319.2	Q45686	G45686 entereococo
956	6	0.8	319.2	Q45686	G45686 entereococo
957	6	0.8	319.2	Q45686	G45686 entereococo
958	6	0.8	319.2	Q45686	G45686 entereococo
959	6	0.8	319.2	Q45686	G45686 entereococo
960	6	0.8	319.2	Q45686	G45686 entereococo
961	6	0.8	319.2	Q45686	G45686 entereococo
962	6	0.8	319.2	Q45686	G45686 entereococo
963	6	0.8	319.2	Q45686	G45686 entereococo
964	6	0.8	319.2	Q45686	G45686 entereococo
965	6	0.8	319.2	Q45686	G45686 entereococo
966	6	0.8	319		

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841	6	0	8	319	10	Q9M236	Q9M236	arabidopsis
842	6	0	8	320	10	Q9M232	Q9M232	arabidopsis
843	6	0	8	321	10	Q9M233	Q9M233	arabidopsis
844	6	0	8	322	10	Q9M234	Q9M234	arabidopsis
845	6	0	8	323	10	Q9M235	Q9M235	arabidopsis
846	6	0	8	324	10	Q9M236	Q9M236	arabidopsis
847	6	0	8	325	10	Q9M237	Q9M237	arabidopsis
848	6	0	8	326	10	Q9M238	Q9M238	arabidopsis
849	6	0	8	327	10	Q9M239	Q9M239	arabidopsis
850	6	0	8	328	10	Q9M240	Q9M240	arabidopsis
851	6	0	8	329	10	Q9M241	Q9M241	arabidopsis
852	6	0	8	330	10	Q9M242	Q9M242	arabidopsis
853	6	0	8	330	2	Q9M243	Q9M243	arabidopsis
854	6	0	8	330	5	Q9M243	Q9M243	arabidopsis
855	6	0	8	330	11	P70271	P70271	arabidopsis
856	6	0	8	331	2	Q9M244	Q9M244	arabidopsis
857	6	0	8	331	2	Q9M244	Q9M244	arabidopsis
858	6	0	8	331	2	Q9M244	Q9M244	arabidopsis
859	6	0	8	331	2	Q9M244	Q9M244	arabidopsis
860	6	0	8	332	4	Q15242	Q15242	homo sapiens
861	6	0	8	332	5	Q4A895	Q4A895	caenorhabditis
862	6	0	8	332	5	Q9V9X2	Q9V9X2	arabidopsis
863	6	0	8	332	5	Q9V9X2	Q9V9X2	arabidopsis
864	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
865	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
866	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
867	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
868	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
869	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
870	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
871	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
872	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
873	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
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875	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
876	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
877	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
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886	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
887	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
888	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
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890	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
891	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
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893	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
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896	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
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898	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
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900	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
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910	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
911	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
912	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
913	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
914	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
915	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
916	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
917	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
918	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
919	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
920	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
921	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
922	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
923	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
924	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
925	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
926	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
927	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
928	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
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930	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
931	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
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933	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
934	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
935	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
936	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
937	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
938	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
939	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
940	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
941	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
942	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
943	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
944	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
945	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
946	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
947	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
948	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
949	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
950	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
951	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
952	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
953	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
954	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
955	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
956	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
957	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
958	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
959	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
960	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
961	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
962	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
963	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
964	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
965	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
966	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
967	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
968	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
969	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
970	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
971	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
972	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
973	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
974	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
975	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
976	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
977	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
978	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
979	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
980	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
981	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
982	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
983	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
984	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
985	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
986	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
987	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
988	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
989	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
990	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
991	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
992	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
993	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
994	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
995	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
996	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
997	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
998	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
999	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m
1000	6	0	8	333	2	Q9K1P0	Q9K1P0	teissiera m

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865	6	0.8	13.3	2	093NM0	OS9M0	nelestriia
866	6	0.8	13.3	5	P93139	P93139	nelestriia
867	6	0.8	13.4	1	093046	093046	pirococcia
868	6	0.8	13.4	1	093046	093046	stireococcia
869	6	0.8	13.4	2	093046	093046	stireococcia
870	6	0.8	13.4	2	093046	093046	stireococcia
871	6	0.8	13.5	2	094268	094268	atomomera s
872	6	0.8	13.5	2	093065	093065	salmonella
873	6	0.8	13.5	5	093062	093062	salmonella
874	6	0.8	13.5	10	093061	093061	salmonella
875	6	0.8	13.5	10	093061	093061	salmonella
876	6	0.8	13.6	2	025910	025910	Helicobacter
877	6	0.8	13.6	2	093041	093041	Helicobacter
878	6	0.8	13.6	2	093041	093041	Helicobacter
879	6	0.8	13.7	3	093070	093070	Helicobacter
880	6	0.8	13.7	11	055219	055219	Helicobacter
881	6	0.8	13.9	2	010324	010324	caldococcus
882	6	0.8	13.9	2	025805	025805	caldococcus
883	6	0.8	13.9	2	025805	025805	caldococcus
884	6	0.8	13.9	4	054905	054905	homo sapien
885	6	0.8	13.9	5	077146	077146	homo sapien
886	6	0.8	14.0	2	045074	045074	homo sapien
887	6	0.8	14.0	2	045074	045074	homo sapien
888	6	0.8	14.0	5	093017	093017	Ceromonab
889	6	0.8	14.1	4	093076	093076	homo sapien
890	6	0.8	14.1	5	018615	018615	Ceromonab
891	6	0.8	14.1	10	093095	093095	acidobacter
892	6	0.8	14.1	10	093095	093095	acidobacter
893	6	0.8	14.1	2	093283	093283	acidobacter
894	6	0.8	14.2	2	093288	093288	hamophilus
895	6	0.8	14.2	2	093288	093288	hamophilus
896	6	0.8	14.2	2	093288	093288	hamophilus
897	6	0.8	14.2	2	093288	093288	hamophilus
898	6	0.8	14.2	2	093288	093288	hamophilus
899	6	0.8	14.2	2	093288	093288	hamophilus
900	6	0.8	14.2	2	093288	093288	hamophilus
901	6	0.8	14.2	2	093288	093288	hamophilus
902	6	0.8	14.2	2	093288	093288	hamophilus
903	6	0.8	14.2	2	093288	093288	hamophilus
904	6	0.8	14.2	2	093288	093288	hamophilus
905	6	0.8	14.2	2	093288	093288	hamophilus
906	6	0.8	14.2	2	093288	093288	hamophilus
907	6	0.8	14.2	2	093288	093288	hamophilus
908	6	0.8	14.2	2	093288	093288	hamophilus
909	6	0.8	14.2	2	093288	093288	hamophilus
910	6	0.8	14.2	2	093288	093288	hamophilus
911	6	0.8	14.2	2	093288	093288	hamophilus
912	6	0.8	14.2	2	093288	093288	hamophilus
913	6	0.8	14.2	2	093288	093288	hamophilus
914	6	0.8	14.2	2	093288	093288	hamophilus
915	6	0.8	14.2	2	093288	093288	hamophilus

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916	6	0	0	8	345	1	Q9YBW2	Q9YBW2 acetylornithin
917	6	0	0	8	345	4	Q9UN47	Q9UN47 homo sapiens
918	6	0	0	8	345	8	P92533	P92533 mahuya arctis
919	6	0	0	8	345	8	P92533	P92533 mahuya arctis
920	6	0	0	8	345	10	Q9A314	Q9A314 Gensu vills vinn
921	6	0	0	8	346	2	Q9E617	Q9E617 aquilex acq
922	6	0	0	8	346	2	Q9ZK25	Q9ZK25 neisseria m
923	6	0	0	8	346	2	Q9R833	Q9R833 neisseria m
924	6	0	0	8	346	2	Q9R832	Q9R832 neisseria m
925	6	0	0	8	346	2	Q9R833	Q9R833 neisseria m
926	6	0	0	8	346	2	Q9R834	Q9R834 xilerycomyc
927	6	0	0	8	346	2	Q9R8B6	Q9R8B6 streptococ
928	6	0	0	8	346	8	P92157	P92157 letricosint
929	6	0	0	8	346	8	Q9RUV7	Q9RUV7 letricosint
930	6	0	0	8	346	8	Q9RUV7	Q9RUV7 letricosint
931	6	0	0	8	346	10	Q9EX91	Q9EX91 arbidodopa
932	6	0	0	8	347	2	Q10563	Q10563 neisseria
933	6	0	0	8	347	2	Q10563	Q10563 neisseria
934	6	0	0	8	347	2	Q99J20	Q99J20 neisseria
935	6	0	0	8	347	2	Q9R833	Q9R833 neisseria
936	6	0	0	8	347	2	Q99J20	Q99J20 neisseria
937	6	0	0	8	347	12	Q9JUB8	Q9JUB8 human lam
938	6	0	0	8	348	2	Q15617	Q15617 borrelia b
939	6	0	0	8	348	7	Q13387	Q13387 neisseria m
940	6	0	0	8	349	2	Q9R8B6	Q9R8B6 streptococ
941	6	0	0	8	349	2	Q9R8B6	Q9R8B6 streptococ
942	6	0	0	8	349	2	Q9R8B6	Q9R8B6 streptococ
943	6	0	0	8	349	10	Q9A145	Q9A145 arbidodopa
944	6	0	0	8	349	10	Q9A145	Q9A145 arbidodopa
945	6	0	0	8	350	2	Q15703	Q15703 neisseria
946	6	0	0	8	350	2	Q151239	Q151239 neisseria
947	6	0	0	8	350	2	Q151244	Q151244 neisseria
948	6	0	0	8	350	2	Q151244	Q151244 neisseria
949	6	0	0	8	350	2	Q9R8B6	Q9R8B6 streptococ
950	6	0	0	8	350	2	Q9R8B6	Q9R8B6 streptococ
951	6	0	0	8	350	2	Q9R8B6	Q9R8B6 streptococ
952	6	0	0	8	350	2	Q9R8B6	Q9R8B6 streptococ
953	6	0	0	8	350	2	Q9R8B6	Q9R8B6 streptococ
954	6	0	0	8	350	5	Q15698	Q15698 chemorinb
955	6	0	0	8	351	2	Q151237	Q151237 neisseria
956	6	0	0	8	351	2	Q9ZAN0	Q9ZAN0 neisseria
957	6	0	0	8	351	2	Q9ZAN0	Q9ZAN0 neisseria
958	6	0	0	8	351	2	Q9ZAN0	Q9ZAN0 neisseria
959	6	0	0	8	351	2	Q9ZAN0	Q9ZAN0 neisseria
960	6	0	0	8	351	2	Q9ZAN0	Q9ZAN0 neisseria
961	6	0	0	8	351	2	Q9ZAN0	Q9ZAN0 neisseria
962	6	0	0	8	351	2	Q9ZAN0	Q9ZAN0 neisseria
963	6	0	0	8	351	2	Q9ZAN0	Q9ZAN0 neisseria
964	6	0	0	8	351	2	Q9ZAN0	Q9ZAN0 neisseria
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968	6	0	0	8	351	2	Q9ZAN0	Q9ZAN0 neisseria
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BL Science 287:1809-1815(2000).  
DR EMBL: A602518; AAF42023.1; -  
DR TIGR: NM1881; -  
KW Hypothetical protein.  
SQ SOURCE 141 AA; ACAAEP529756063 CIRC64;

Query Match 1.1%; Score 8; DB 2; Length 141;  
Best Local Similarity 100.0%; Pred. No. 6.1;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 696 QAAETLS 703  
DB 122 QAAETLS 129

RESULT 15

085681 PRELIMINARY; PRT; 162 AA.

AC Q95681; 11

DT 01-NOV-1998 (TRIMBLrel. 08; Created)

DT 01-NOV-1998 (TRIMBLrel. 12; Last sequence update)

DT 01-OCT-2000 (TRIMBLrel. 15; Last annotation update)

DE HYPOHYPOTHECAL 17.1 KDa PROTEIN (PNAOENMT)

OS Streptomyces glaucus

OC Bacteria; Firmicutes; Actinobacteria; Actinomycetales;

OC Actinomycetales; Streptomyces; Streptomyces; Streptomyces;

NCBI\_TaxID=7833

RP SEQUENCE FROM N.A.

RA Kim S.O., Hyun C.G., Suh J.M.;

RT Efficient cloning of the genes for RNA polymerase sigma-like factors

RL J. Microbiol. Biotechnol. 8:280-283(1998).

DR EMBL: AF01793; AAC2685.1; -

DR HSPF; P00579; 1556;

DR P00579; 1556;

DR P00579; 1556;

DR P00579; 1556;

DR P00579; 1556;

DR P00579; 1556;

DR P00579; 1556;

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DR P00579; 1556;

DR P00579; 1556;

DR P00579; 1556;

BL Science 287:1809-1815(2000).  
DR EMBL: A602518; AAF42023.1; -  
DR TIGR: NM1881; -  
KW Hypothetical protein.  
SQ SOURCE 141 AA; ACAAEP529756063 CIRC64;

Query Match 1.1%; Score 8; DB 4; Length 165;  
Best Local Similarity 100.0%; Pred. No. 7.1;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 LLEWGS 268  
DB 29 LLEWGS 36

RESULT 16

09X198 PRELIMINARY; PRT; 256 AA.

AC Q9X198; 11

DT 01-NOV-1998 (TRIMBLrel. 12; Created)

DT 01-NOV-1998 (TRIMBLrel. 12; Last sequence update)

DT 01-OCT-2000 (TRIMBLrel. 15; Last annotation update)

DE HYPOHYPOTHECAL 17.1 KDa PROTEIN (PNAOENMT)

OS Streptomyces glaucus

OC Bacteria; Firmicutes; Actinobacteria; Actinomycetales;

OC Actinomycetales; Streptomyces; Streptomyces; Streptomyces;

NCBI\_TaxID=7833

RP SEQUENCE FROM N.A.

RA Kim S.O., Hyun C.G., Suh J.M.;

RT Efficient cloning of the genes for RNA polymerase sigma-like factors

RL J. Microbiol. Biotechnol. 8:280-283(1998).

DR EMBL: AF01793; AAC2685.1; -

DR HSPF; P00579; 1556;

DR P00579; 1556;

DR P00579; 1556;

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DR P00579; 1556;













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D7      01-NOV-1998 (TREMBL) 1, Last sequence update)
D8      01-OCT-2000 (TREMBL) 15, Last annotation update)
D9      01-SEP-2000 (TREMBL) 16, Last annotation update)
DB      PROTEIN KANSASOBS (Protein).
CN      SRCA
OC      Prochloron diatomii.
ON      [?].
NC      Bacteria:Cyanobacteria: Prochlorophytes: Prochlorococcus: Prochloron.
NM      [?].
NN      [?].
NP      SEQUENCE FROM N.A.
RA      Barb Brook A.C.;
RB      Submitted (MAR-1999) to the EMBL/Genbank/UDBA database.
RC      [?].
RD      [?].
RE      [?].
RF      [?].
RG      [?].
RH      [?].
RI      [?].
RJ      [?].
RK      [?].
RL      Rheebs (1986); University of Cambridge, Cambridge, UK.
RM      [?].
RN      INTERPRO:IPRO00185, I258.1, -.
RO      PRAM; P201043; SecA_Protein; 1.
RP      PRINTS: PR00906; SECN.
RQ      NON-TER 266 266
RS      SEQUENCE 266 AA; 30186 MW; A6F4FAE8B5317E CRC64;
SQ      Query Match 1.0%; Score 7; DB 2; Length 266;
        Best Local Similarity 100.0%; Pred No. 1.1e+02;
        Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0
DY      355 SLLGRD 401
        111111
DB      227 SLLGRD 233

RESULT 45
ID C82397 PRELIMINARY: PTY: 284 AA.
AC C82397; 1998 (TRENDEL) 08, Great sequence update)
AD 01-NOV-1998 (TREMBL) 08, Last sequence update)
DT 01-JUN-2000 (TREMBL) 14, Last annotation update)
DB HYPOTHEZICAL 32.6 kDa PROTEIN.
DN TIO2D 2.
OS [?].
NC [?].
NM [?].
NN [?].
NP [?].
RA [?].
RB [?].
RC [?].
RD [?].
RE [?].
RF [?].
RG [?].
RH [?].
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RO [?].
RP [?].
RQ [?].
RS [?].
SQ [?].

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[illegible][illegible][illegible]

[illegible]

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Mon Apr 9 11:14:16 2001                                     us-08-403-803-z_cowp_45_750_011g.fpcpt

Query Match          1.0%      Score 7, DB 5, Length 313;
Best Local Similarity 100.0%;   Pred. No. 1, Size 02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qz           370 RTIFRS 376
            |||||||
Db           91 RTIFRS 97

RESULT 50
COA114
ID COA114             PRELIMINARY: PRT. 317 AA.
DT 01-NOV-1996 (TEMBELrel. 01, Created)
DT 01-NOV-1996 (TEMBELrel. 01, Last sequence update)
DT 01-JAN-1999 (TEMBELrel. 09, Last annotation update)
CN PRX
PRX PLASMAINT PROTEIN PROX
OS Enterococcus faecalis (Streptococcus faecalis).
OC Firmicutes; Bacillales; Clostridium group; Enterococcaceae;
NCBI Taxid:1351;
OX NCBI_Taxid:1351;
EN [1]
SR SOURCE FROM N.A.
RA Kuo S.M., Olsted S.B., Vikström A.S., Gallo J.C., Dunny G.M.;
RT "Molecular and genetic analysis of a region of plasmid pF10
RT containing positive control genes and structural genes encoding in
RT Enterococcus faecalis." In Phenomenon-Inducible conjugation in
RL R. Bacteriol. 173:7650-7664(1991).
BL EMBL: M64978; AAA65445.1; -
DB PubMed 173650
SQ SEQUENCE 317 AA; 3705 MW; 41165B67816C4AD Check;

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On protein - protein search, using sw model  
 Run on: April 6, 2001, 16:56:42; Search time 13.55 Seconds  
 (without alignments)  
 1687.639 Million cell updates/sec

Title: US-08-403-803-2.copv\_45\_750  
 Perfect score: 706  
 Sequence: 1 SSNATNTPKHNKAPLDE.....QIVYAFVQAMETLSPVA 706  
 Scoring table: Q1000  
 Gap: 60.0, Gapext: 60.0  
 Searched: 88757 seqs, 32294092 residues  
 Word size: 6  
 Total number of hits satisfying chosen parameters: 905  
 Minimum DB seq length: 0  
 Maximum DB seq length: 200000000  
 Post-processing: Listing first 1000 summaries  
 Database: SwissProt\_39\*

Pred. No. is the number of results predicted by chance to have a  
 perfect score. The results are sorted by the probability of being  
 and is derived by analysis of the total score distribution.

Result	No.	Score	Match	Length	DB ID	Description
	2	706	100.0	706	1202	1 PPM2_YEAST
	3	706	100.0	706	64	1 PPM2_YEAST
	4	706	100.0	706	92	1 Y108_SSV1
	5	706	100.0	706	102	1 PPM2_YEAST
	6	706	100.0	706	102	1 PPM2_YEAST
	7	706	100.0	706	124	1 UNR2_LACPE
	8	706	100.0	706	124	1 UNR2_LACPE
	9	706	100.0	706	124	1 UNR2_LACPE
	10	706	100.0	706	124	1 UNR2_LACPE
	11	706	100.0	706	124	1 UNR2_LACPE
	12	706	100.0	706	124	1 UNR2_LACPE
	13	706	100.0	706	124	1 UNR2_LACPE
	14	706	100.0	706	124	1 UNR2_LACPE
	15	706	100.0	706	124	1 UNR2_LACPE
	16	706	100.0	706	124	1 UNR2_LACPE
	17	706	100.0	706	124	1 UNR2_LACPE
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48	7	1.0	251	1	BS04_YEAST	P32905 saccharomy
49	7	1.0	251	1	BS04_YEAST	P32905 saccharomy
50	7	1.0	251	1	BS04_YEAST	P32905 saccharomy
51	7	1.0	251	1	BS04_YEAST	P32905 saccharomy
52	7	1.0	251	1	BS04_YEAST	P32905 saccharomy
53	7	1.0	251	1	BS04_YEAST	P32905 saccharomy
54	7	1.0	251	1	BS04_YEAST	P32905 saccharomy
55	7	1.0	251	1	BS04_YEAST	P32905 saccharomy
56	7	1.0	251	1	BS04_YEAST	P32905 saccharomy
57	7	1.0	251	1	BS04_YEAST	P32905 saccharomy
58	7	1.0	251	1	BS04_YEAST	P32905 saccharomy
59	7	1.0	251	1	BS04_YEAST	P32905 saccharomy
60	7	1.0	251	1	BS04_YEAST	P32905 saccharomy
61	7	1.0	251	1	BS04_YEAST	P32905 saccharomy
62	7	1.0	251	1	BS04_YEAST	P32905 saccharomy

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[illegible]

216	6	0	8	287	1	LEP1_XNXP	Q56763	keithinase
217	6	0	8	290	1	PRI1_XNXP	P71203	synthetase
218	6	0	8	294	1	DMR_AOAE	Q62146	antifungal
219	6	0	8	296	1	NTR1_BDOL	Q00240	pectinase
220	6	0	8	298	1	EXS1_OSAE	Q26903	penicillinase
221	6	0	8	300	1	CHG1_SYMP	P18834	synthetase
222	6	0	8	300	1	YATE_RHIN	P55569	ribitolium
223	6	0	8	300	1	KCT1_LAMN	Q61801	hemophillin
224	6	0	8	302	1	PIX1_MORF	Q3160	mts aminotransferase
225	6	0	8	302	1	PIX1_MAV	B81062	ratlun not
226	6	0	8	305	1	RIE1_SYNY	P71432	synthetase
227	6	0	8	306	1	RIE1_BDOL	P43322	helicin II
228	6	0	8	306	1	YMT1_BDOL	Q46564	lectinase
229	6	0	8	309	1	YMT1_MORF	P53949	mts aminotransferase
230	6	0	8	310	1	SPO1_BDOL	P18827	homo aspartate
231	6	0	8	310	1	YPS1_BDOL	Q53529	metanobacter
232	6	0	8	310	1	YPS1_MORF	Q53529	metanobacter
233	6	0	8	314	1	MYR1_BDOL	P08331	echinotrichin
234	6	0	8	314	1	MYR1_MORF	P08331	echinotrichin
235	6	0	8	317	1	PEP1_PANT	P71580	echinotrichin
236	6	0	8	317	1	PEP1_BDOL	Q62887	ratlun not
237	6	0	8	317	1	PEP1_MORF	P71580	echinotrichin
238	6	0	8	318	1	ACD1_BDOL	P55339	ribitolium
239	6	0	8	320	1	ACD1_MORF	P55339	ribitolium
240	6	0	8	322	1	MOD1_RHIN	P13728	ribitolium
241	6	0	8	322	1	MOD1_MORF	P13728	ribitolium
242	6	0	8	323	1	SHB1_SYNY	Q33463	synthetase
243	6	0	8	323	1	SHB1_BDOL	P13727	pectinase
244	6	0	8	323	1	NOI1_PANT	Q10685	mycobacter
245	6	0	8	323	1	YF71_MORF	Q50728	mycobacter
246	6	0	8	323	1	YF71_BDOL	P34590	cephalosporin
247	6	0	8	325	1	YF61_MORF	Q50728	mycobacter
248	6	0	8	325	1	YF61_BDOL	P34590	cephalosporin
249	6	0	8	326	1	YF51_MORF	P75316	echinotrichin
250	6	0	8	327	1	CHG2_PANT	P75316	echinotrichin
251	6	0	8	328	1	EXD1_BDOL	P26503	ribitolium
252	6	0	8	328	1	EXD1_MORF	P26503	ribitolium
253	6	0	8	328	1	ORY1_MORF	P51476	lectinase
254	6	0	8	328	1	ORY1_BDOL	P51476	lectinase
255	6	0	8	328	1	STY1_MORF	P26503	ribitolium
256	6	0	8	328	1	STY1_BDOL	P26503	ribitolium
257	6	0	8	330	1	MYR1_BDOL	P26503	ribitolium
258	6	0	8	331	1	MYR1_MORF	P26503	ribitolium
259	6	0	8	331	1	PIR1_MORF	Q28966	archaeoglobulin
260	6	0	8	332	1	IND1_MORF	P41632	mts aminotransferase
261	6	0	8	332	1	IND1_BDOL	P41632	mts aminotransferase
262	6	0	8	332	1	THC1_MORF	P41632	ribitolium
263	6	0	8	332	1	THC1_BDOL	P41632	ribitolium

267	0.8	3.33	1	OCN1_ZBOAT
268	0.8	3.33	1	TAL_ZBOAT
269	0.8	3.33	1	TRP_ZBOAT
270	0.8	3.37	1	R1R2_ZRFB
271	0.8	3.37	1	V1N1_ZP2
272	0.8	3.38	1	TRP_ZRFB
273	0.8	3.38	1	TRP_ZRFB
274	0.8	3.39	1	CRN_ZRFB
275	0.8	3.40	1	ADK_ZRFB
276	0.8	3.40	1	ADK_ZRFB
277	0.8	3.41	1	STW_ZCOST
278	0.8	3.41	1	STW_ZCOST
279	0.8	3.42	1	LOM_ZBOV1
280	0.8	3.42	1	MORR_ZBOV1
281	0.8	3.44	1	MRG_ZMOSE
282	0.8	3.44	1	MRG_ZMOSE
283	0.8	3.45	1	STED_ZJN1N
284	0.8	3.45	1	AMP_ZMOSE
285	0.8	3.49	1	ISL_ZRFB
286	0.8	3.49	1	ISL_ZRFB
287	0.8	3.49	1	ISL_ZRFB
288	0.8	3.51	1	PLNC_PEN11
289	0.8	3.51	1	PLNC_PEN11
290	0.8	3.51	1	U105_ZSYNG
291	0.8	3.52	1	MDM_ZRFB
292	0.8	3.52	1	MDM_ZRFB
293	0.8	3.53	1	V475_ZR1N
294	0.8	3.53	1	YOCU_ZRFB
295	0.8	3.53	1	YOCU_ZRFB
296	0.8	3.55	1	R1B_ZRFB
297	0.8	3.56	1	R1B_ZRFB
298	0.8	3.56	1	R1B_ZRFB
299	0.8	3.55	1	U198_ZRFB
300	0.8	3.57	1	LOA_ZRFB
301	0.8	3.58	1	LOA_ZRFB
302	0.8	3.58	1	LOA_ZRFB
303	0.8	3.58	1	LOA_ZRFB
304	0.8	3.58	1	LOA_ZRFB
305	0.8	3.60	1	MSB_ZLACT
306	0.8	3.60	1	MSB_ZLACT
307	0.8	3.60	1	MSB_ZLACT
308	0.8	3.63	1	LYA2_ZRFB
309	0.8	3.63	1	LYA2_ZRFB
310	0.8	3.66	1	TRP_ZRFB
311	0.8	3.66	1	TRP_ZRFB
312	0.8	3.67	1	DOS1_ZMOSE
313	0.8	3.67	1	DOS1_ZRFB
314	0.8	3.67	1	DOS1_ZRFB
315	0.8	3.68	1	VE2_ZRFB
316	0.8	3.70	1	5H8_ZRFB
317	0.8	3.70	1	5H8_ZRFB
318	0.8	3.70	1	5H8_ZRFB
319	0.8	3.70	1	5H8_ZRFB
320	0.8	3.70	1	5H8_ZRFB
321	0.8	3.70	1	5H8_ZRFB
322	0.8	3.70	1	5H8_ZRFB
323	0.8	3.70	1	5H8_ZRFB
324	0.8	3.70	1	5H8_ZRFB
325	0.8	3.70	1	5H8_ZRFB
326	0.8	3.70	1	5H8_ZRFB
327	0.8	3.70	1	5H8_ZRFB
328	0.8	3.70	1	5H8_ZRFB
329	0.8	3.70	1	5H8_ZRFB
330	0.8	3.70	1	5H8_ZRFB
331	0.8	3.70	1	5H8_ZRFB
332	0.8	3.70	1	5H8_ZRFB
333	0.8	3.70	1	5H8_ZRFB
334	0.8	3.70	1	5H8_ZRFB
335	0.8	3.70	1	5H8_ZRFB
336	0.8	3.70	1	5H8_ZRFB
337	0.8	3.70	1	5H8_ZRFB
338	0.8	3.70	1	5H8_ZRFB
339	0.8	3.70	1	5H8_ZRFB
340	0.8	3.70	1	5H8_ZRFB
341	0.8	3.70	1	5H8_ZRFB
342	0.8	3.70	1	5H8_ZRFB
343	0.8	3.70	1	5H8_ZRFB
344	0.8	3.70	1	5H8_ZRFB
345	0.8	3.70	1	5H8_ZRFB
346	0.8	3.70	1	5H8_ZRFB
347	0.8	3.70	1	5H8_ZRFB
348	0.8	3.70	1	5H8_ZRFB
349	0.8	3.70	1	5H8_ZRFB
350	0.8	3.70	1	5H8_ZRFB
351	0.8	3.70	1	5H8_ZRFB
352	0.8	3.70	1	5H8_ZRFB
353	0.8	3.70	1	5H8_ZRFB
354	0.8	3.70	1	

318	6	0.8	371	1	MALC_MERAO
319	6	0.8	372	1	3MH_MERAO
320	6	0.8	373	1	3MH_MERAO
321	6	0.8	374	1	WALC_MERAO
322	6	0.8	375	1	WALC_MERAO
323	6	0.8	376	1	WALC_MERAO
324	6	0.8	377	1	WALC_MERAO
325	6	0.8	378	1	WALC_MERAO
326	6	0.8	379	1	WALC_MERAO
327	6	0.8	380	1	WALC_MERAO
328	6	0.8	381	1	WALC_MERAO
329	6	0.8	382	1	WALC_MERAO
330	6	0.8	383	1	WALC_MERAO
331	6	0.8	384	1	WALC_MERAO
332	6	0.8	385	1	WALC_MERAO
333	6	0.8	386	1	WALC_MERAO
334	6	0.8	387	1	WALC_MERAO
335	6	0.8	388	1	WALC_MERAO
336	6	0.8	389	1	WALC_MERAO
337	6	0.8	390	1	WALC_MERAO
338	6	0.8	391	1	WALC_MERAO
339	6	0.8	392	1	WALC_MERAO
340	6	0.8	393	1	WALC_MERAO
341	6	0.8	394	1	WALC_MERAO
342	6	0.8	395	1	WALC_MERAO
343	6	0.8	396	1	WALC_MERAO
344	6	0.8	397	1	WALC_MERAO
345	6	0.8	398	1	WALC_MERAO
346	6	0.8	399	1	WALC_MERAO
347	6	0.8	400	1	WALC_MERAO
348	6	0.8	401	1	WALC_MERAO
349	6	0.8	402	1	WALC_MERAO
350	6	0.8	403	1	WALC_MERAO
351	6	0.8	404	1	WALC_MERAO
352	6	0.8	405	1	WALC_MERAO
353	6	0.8	406	1	WALC_MERAO
354	6	0.8	407	1	WALC_MERAO
355	6	0.8	408	1	WALC_MERAO
356	6	0.8	409	1	WALC_MERAO
357	6	0.8	410	1	WALC_MERAO
358	6	0.8	411	1	WALC_MERAO
359	6	0.8	412	1	WALC_MERAO
360	6	0.8	413	1	WALC_MERAO
361	6	0.8	414	1	WALC_MERAO
362	6	0.8	415	1	WALC_MERAO
363	6	0.8	416	1	WALC_MERAO
364	6	0.8	417	1	WALC_MERAO
365	6	0.8	418	1	WALC_MERAO
366	6	0.8	419	1	WALC_MERAO
367	6	0.8	420	1	WALC_MERAO
368	6	0.8	421	1	WALC_MERAO
369	6	0.8	422	1	WALC_MERAO
370	6	0.8	423	1	WALC_MERAO
371	6	0.8	424	1	WALC_MERAO
372	6	0.8	425	1	WALC_MERAO
373	6	0.8	426	1	WALC_MERAO
374	6	0.8	427	1	WALC_MERAO
375	6	0.8	428	1	WALC_MERAO
376	6	0.8	429	1	WALC_MERAO
377	6	0.8	430	1	WALC_MERAO
378	6	0.8	431	1	WALC_MERAO
379	6	0.8	432	1	WALC_MERAO
380	6	0.8	433	1	WALC_MERAO
381	6	0.8	434	1	WALC_MERAO
382	6	0.8	435	1	WALC_MERAO
383	6	0.8	436	1	WALC_MERAO
384	6	0.8	437	1	WALC_MERAO
385	6	0.8	438	1	WALC_MERAO
386	6	0.8	439	1	WALC_MERAO
387	6	0.8	440	1	WALC_MERAO
388	6	0.8	441	1	WALC_MERAO
389	6	0.8	442	1	WALC_MERAO
390	6	0.8	443	1	WALC_MERAO
391	6	0.8	444	1	WALC_MERAO
392	6	0.8	445	1	WALC_MERAO
393	6	0.8	446	1	WALC_MERAO
394	6	0.8	447	1	WALC_MERAO
395	6	0.8	448	1	WALC_MERAO
396	6	0.8	449		

359	6	0.8	415	1	SVS_HELP4	Q93493	helicobacter
370	6	0.8	415	1	SVS_HELP4	P56456	helicobacter
371	6	0.8	416	1	CGC_CLOCK	Q12033	glicinae mus
372	6	0.8	417	1	MSL_HUMAN	Q93038	h wsl.1-pro
373	6	0.8	417	1	GLBZ_ECOLI	P12313	escherichia
374	6	0.8	419	1	HEMZ_MOUSE	P12313	mus musculus
375	6	0.8	420	1	HEMZ_MOUSE	P12313	mus musculus
376	6	0.8	421	1	CHT_TITIL	P48827	trichodroma
377	6	0.8	421	1	CHT_TITIL	P48827	trichodroma
378	6	0.8	423	1	TYD_HUMAN	P26440	homo sapien
379	6	0.8	427	1	DSXF_ECOLI	P15022	drosophila
380	6	0.8	429	1	URNA_ECOLI	P12360	escherichia
381	6	0.8	430	1	LEP2_MOUSE	Q01015	hempiparus
382	6	0.8	430	1	LEP2_MOUSE	Q01015	hempiparus
383	6	0.8	432	1	LEP2_MOUSE	Q01015	hempiparus
384	6	0.8	432	1	NPFL_MOUSE	Q52443	mus musculus
385	6	0.8	433	1	WPMN_SCTC	Q31180	mycobacter
386	6	0.8	433	1	WPMN_SCTC	Q31180	mycobacter
387	6	0.8	435	1	BAZ2_RIOLA	P16766	kluweyeana
388	6	0.8	437	1	SEPG_HUMAN	P36641	homo sapien
389	6	0.8	437	1	SEPG_HUMAN	P36641	homo sapien
390	6	0.8	437	1	SEPG_HUMAN	P36641	homo sapien
391	6	0.8	437	1	PRF4_TAST	P40327	macromony
392	6	0.8	437	1	PRF4_TAST	P40327	macromony
393	6	0.8	439	1	PRF4_TAST	P40327	macromony
394	6	0.8	439	1	PRF4_TAST	P40327	macromony
395	6	0.8	440	1	PRF4_TAST	P40327	macromony
396	6	0.8	440	1	PRF4_TAST	P40327	macromony
397	6	0.8	440	1	PRF4_TAST	P40327	macromony
398	6	0.8	440	1	PRF4_TAST	P40327	macromony
399	6	0.8	441	1	PRF4_TAST	P40327	macromony
400	6	0.8	441	1	PRF4_TAST	P40327	macromony
401	6	0.8	442	1	TNMC_BACSU	P37623	baecillus aeo
402	6	0.8	443	1	PRF4_ECOLI	O16166	canonrhabeid
403	6	0.8	444	1	TYAC_STYLO	P472039	canonrhabeid
404	6	0.8	446	1	PRF4_TAST	P23166	tylomonchias
405	6	0.8	447	1	TYMB_BOEIL	P55680	helicobium a
406	6	0.8	447	1	TYMB_BOEIL	P45526	helicobium a
407	6	0.8	448	1	PRF4_TAST	P36512	schistosoma
408	6	0.8	448	1	PRF4_TAST	P36512	schistosoma
409	6	0.8	449	1	CEPL_MCFR	P33266	schistosoma
410	6	0.8	449	1	GND_MOUSE	P12293	mus musculus
411	6	0.8	449	1	GND_MOUSE	P12293	mus musculus
412	6	0.8	449	1	GND_MOUSE	P12293	mus musculus
413	6	0.8	450	1	YFEB_BACSU	P38490	baecillus aeo
414	6	0.8	451	1	YFEB_BACSU	Q04899	mus musculus
415	6	0.8	451	1	KRT1_TAST	P35872	ratellus norv
416	6	0.8	451	1	KRT1_TAST	P35872	ratellus norv
417	6	0.8	452	1	GND_HUMAN	O14764	homo sapien
418	6	0.8	452	1	GND_HUMAN	P08194	schistosoma
419	6	0.8	452	1	TYTP_BOEIL	P48613	schistosoma
420	6	0.8	452	1	TYTP_BOEIL	P48613	schistosoma

420	6	0	0	8	433	1	GNAT_HELPD
421	6	0	0	8	433	1	GNAT_HELPD
422	6	0	0	8	433	1	GNAT_HELPD
423	6	0	0	8	453	1	GNAT_HELPD
424	6	0	0	8	453	1	GNAT_HELPD
425	6	0	0	8	453	1	GNAT_HELPD
426	6	0	0	8	456	1	GNAT_HELPD
427	6	0	0	8	456	1	GNAT_HELPD
428	6	0	0	8	457	1	GNAT_HELPD
429	6	0	0	8	458	1	GNAT_HELPD
430	6	0	0	8	458	1	GNAT_HELPD
431	6	0	0	8	461	1	GNAT_HELPD
432	6	0	0	8	461	1	GNAT_HELPD
433	6	0	0	8	461	1	GNAT_HELPD
434	6	0	0	8	464	1	GNAT_HELPD
435	6	0	0	8	464	1	GNAT_HELPD
436	6	0	0	8	465	1	GNAT_HELPD
437	6	0	0	8	465	1	GNAT_HELPD
438	6	0	0	8	465	1	GNAT_HELPD
439	6	0	0	8	465	1	GNAT_HELPD
440	6	0	0	8	470	1	GNAT_HELPD
441	6	0	0	8	470	1	GNAT_HELPD
442	6	0	0	8	470	1	GNAT_HELPD
443	6	0	0	8	471	1	GNAT_HELPD
444	6	0	0	8	471	1	GNAT_HELPD
445	6	0	0	8	471	1	GNAT_HELPD
446	6	0	0	8	471	1	GNAT_HELPD
447	6	0	0	8	471	1	GNAT_HELPD
448	6	0	0	8	471	1	GNAT_HELPD
449	6	0	0	8	476	1	GNAT_HELPD
450	6	0	0	8	477	1	GNAT_HELPD
451	6	0	0	8	477	1	GNAT_HELPD
452	6	0	0	8	478	1	GNAT_HELPD
453	6	0	0	8	478	1	GNAT_HELPD
454	6	0	0	8	478	1	GNAT_HELPD
455	6	0	0	8	478	1	GNAT_HELPD
456	6	0	0	8	478	1	GNAT_HELPD
457	6	0	0	8	481	1	GNAT_HELPD
458	6	0	0	8	481	1	GNAT_HELPD
459	6	0	0	8	485	1	GNAT_HELPD
460	6	0	0	8	485	1	GNAT_HELPD
461	6	0	0	8	485	1	GNAT_HELPD
462	6	0	0	8	489	1	GNAT_HELPD
463	6	0	0	8	489	1	GNAT_HELPD
464	6	0	0	8	490	1	GNAT_HELPD
465	6	0	0	8	490	1	GNAT_HELPD
466	6	0	0	8	490	1	GNAT_HELPD
467	6	0	0	8	492	1	GNAT_HELPD
468	6	0	0	8	493	1	GNAT_HELPD
469	6	0	0	8	493	1	GNAT_HELPD
470	6	0	0	8	493	1	GNAT_HELPD
471	6	0	0	8	493	1	GNAT_HELPD
472	6	0	0	8	493	1	GNAT_HELPD
473	6	0	0	8	493	1	GNAT_HELPD
474	6	0	0	8	493	1	GNAT_HELPD
475	6	0	0	8	493	1	GNAT_HELPD
476	6	0	0	8	493	1	GNAT_HELPD
477	6	0	0	8	493	1	GNAT_HELPD
478	6	0	0	8	493	1	GNAT_HELPD
479	6	0	0	8	493	1	GNAT_HELPD
480	6	0	0	8	493	1	GNAT_HELPD
481	6	0	0	8	493	1	GNAT_HELPD
482	6	0	0	8	493	1	GNAT_HELPD
483	6	0	0	8	493	1	GNAT_HELPD
484	6	0	0	8	493	1	GNAT_HELPD
485	6	0	0	8	493	1	GNAT_HELPD
486	6	0	0	8	493	1	GNAT_HELPD
487	6	0	0	8	493	1	GNAT_HELPD
488							

471	6	0.8	493	1	CHEL_RAT	P08682	CRYOGALIN
472	6	0.8	493	1	CHEL_RAT	P05185	retius novy
473	6	0.8	493	1	PDI_CHICK	P09102	galus gall
474	6	0.8	493	1	BRSA_MOUSE	P44135	haemophilin
475	6	0.8	494	1	AMN1_DROME	P08144	drosophila
476	6	0.8	494	1	AMN1_DROME	P08144	drosophila
477	6	0.8	494	1	AMN1_DROME	P51546	drosophila
478	6	0.8	494	1	AMN1_DROME	P16141	drosophila
479	6	0.8	495	1	CHEL_BOVIN	O19383	nos salicis
480	6	0.8	497	1	ANSP_SALTY	P49013	salmonella
481	6	0.8	497	1	ANSP_SALTY	P49013	salmonella
482	6	0.8	497	1	RP54_PSEU	P49088	pseudomonas
483	6	0.8	497	1	RP54_PSEU	P15554	pseudomonas
484	6	0.8	499	1	ADP1_SCHRO	O59191	schistosoma
485	6	0.8	499	1	ADP1_SCHRO	P08683	retius novy
486	6	0.8	501	1	C7B3_ALBAT	P08683	retius novy
487	6	0.8	502	1	ATPA_CAMEL	O65195	arabidopsis
488	6	0.8	502	1	ATPA_CAMEL	P08683	retius novy
489	6	0.8	506	1	CNTA_DICOR	P03052	aeolobacter
490	6	0.8	506	1	CNTA_DICOR	P10593	euglena gra
491	6	0.8	507	1	CNTA_DROME	P17136	drosophila
492	6	0.8	507	1	PHO1_MYCE	P44145	mycoplasma
493	6	0.8	509	1	PHO1_MYCE	P44145	mycoplasma
494	6	0.8	510	1	PMG1_BACSU	P13977	bacillus su
495	6	0.8	511	1	R1E2_PORPU	P51211	boobypha pu
496	6	0.8	514	1	VMS1_HAEM	P44045	haemophilin
497	6	0.8	515	1	CPT1_ORYLA	P10085	oryzias lat
498	6	0.8	518	1	R1E1_YEAST	P28708	aschochyoma
499	6	0.8	518	1	TPH4_DROME	P49455	drosophila
500	6	0.8	522	1	CATC_DICOL	O10710	istius can
501	6	0.8	522	1	NPPI_MOUSE	O10710	istius can
502	6	0.8	523	1	NPPI_MOUSE	O10710	istius can
503	6	0.8	523	1	NPPI_MOUSE	O10710	istius can
504	6	0.8	523	1	NPPI_MOUSE	O10710	istius can
505	6	0.8	526	1	CNTA_MOUSE	P44270	mus musculus
506	6	0.8	526	1	CNTA_MOUSE	P44270	mus musculus
507	6	0.8	527	1	CNTA_MOUSE	P44270	mus musculus
508	6	0.8	527	1	CNTA_MOUSE	P44270	mus musculus
509	6	0.8	528	1	RAT1_MOUSE	O49678	ratia rosaga
510	6	0.8	528	1	RAT1_MOUSE	O49678	ratia rosaga
511	6	0.8	529	1	VSME_YEASB	P10390	bacteriophag
512	6	0.8	531	1	TDD1_FASFO	P51769	phagep8
513	6	0.8	531	1	UDD1_FASFO	O64633	retius novy
514	6	0.8	532	1	PMOS_MOUSE	P49336	mouse
515	6	0.8	532	1	PMOS_MOUSE	P49336	mouse
516	6	0.8	532	1	PMOS_MOUSE	P49336	mouse
517	6	0.8	532	1	PMOS_MOUSE	P49336	mouse
518	6	0.8	534	1	EPA1_HUMI	P59561	homo sapien
519	6	0.8	535	1	GDI1_HUMI	P28492	retius novy
520	6	0.8	535	1	GDI1_HUMI	P28492	retius novy
521	6	0.8	535	1	MYC10_MYCTO	O10652	mycobacteri

5321	6	0	0	8	539	1	CMB1_BRNA	P77633	bradyrhizobium
5322	6	0	0	8	539	1	L116_CAEH1	G217435	caeniibacter
5323	6	0	0	8	541	1	CMB2_RHME	P15472	rhyliobium
5324	6	0	0	8	541	1	CMB2_RHME	P15472	rhyliobium
5325	6	0	0	8	542	1	CMB2_RHME	P15470	rhyliobium
5326	6	0	0	8	542	1	CMB2_RHME	P15470	rhyliobium
5327	6	0	0	8	542	1	Y1M1_YEAS7	P40174	saccharomyces
5328	6	0	0	8	544	1	RHPO_DPMS2	P00655	bacteriophages
5329	6	0	0	8	544	1	RHPO_DPMS2	P00655	bacteriophages
5330	6	0	0	8	544	1	Y074_SYNY3	P71468	synecococcus
5331	6	0	0	8	547	1	THIC_WCYLE	G95810	synecococcus
5332	6	0	0	8	547	1	THIC_WCYLE	G95810	synecococcus
5333	6	0	0	8	549	1	CMB2_BRNA	P50548	monas
5334	6	0	0	8	549	1	CMB2_BRNA	P50548	monas
5335	6	0	0	8	549	1	DESM_BROME	P33681	bradyrhizobium
5336	6	0	0	8	551	1	CAP_SCHO	P32073	strepptococcus
5337	6	0	0	8	551	1	CAP_SCHO	P32073	strepptococcus
5338	6	0	0	8	551	1	FKC1_RHDAN	P36624	halobacterium
5339	6	0	0	8	554	1	FKC1_RHDAN	P36624	halobacterium
5340	6	0	0	8	554	1	FKC1_RHDAN	P36624	halobacterium
5341	6	0	0	8	554	1	FKC1_RHDAN	P36624	halobacterium
5342	6	0	0	8	555	1	PKC1_DABIT	G12948	monas
5343	6	0	0	8	555	1	PKC1_DABIT	G12948	monas
5344	6	0	0	8	559	1	THRA_S0157	P10792	sea
5345	6	0	0	8	560	1	7F50_S0158	G24734	salicibacter
5346	6	0	0	8	560	1	7F50_S0158	G24734	salicibacter
5347	6	0	0	8	567	1	G6FA_ORCSA	P46613	oryza
5348	6	0	0	8	567	1	G6FA_ORCSA	P46613	oryza
5349	6	0	0	8	569	1	V119_WYCE2	P71835	hycomyces
5350	6	0	0	8	571	1	P1L1_B0CA1	G96416	buchnera
5351	6	0	0	8	573	1	G1P1_YEAS7	P03320	saccharomyces
5352	6	0	0	8	574	1	WGLE_HRSVU	P12568	human
5353	6	0	0	8	574	1	WGLE_HRSVU	P12568	human
5354	6	0	0	8	577	1	SHM1_YEAS7	P33955	saccharomyces
5355	6	0	0	8	577	1	SHM1_YEAS7	P33955	saccharomyces
5356	6	0	0	8	577	1	SHM1_YEAS7	P33955	saccharomyces
5357	6	0	0	8	577	1	SHM1_YEAS7	P33955	saccharomyces
5358	6	0	0	8	578	1	P1L1_STEUS1	P30269	strepptococcus
5359	6	0	0	8	578	1	P1L1_STEUS1	P30269	strepptococcus
5360	6	0	0	8	578	1	ACG2_STEKO	P44105	strepptococcus
5361	6	0	0	8	578	1	ACG2_STEKO	P44105	strepptococcus
5362	6	0	0	8	578	1	ACG2_STEKO	P44105	strepptococcus
5363	6	0	0	8	584	1	AYFA_MERBA	P23187	rhodospirillum
5364	6	0	0	8	584	1	AYFA_MERBA	P23187	rhodospirillum
5365	6	0	0	8	584	1	AYFA_MERBA	P23187	rhodospirillum
5366	6	0	0	8	584	1	AYFA_MERBA	P23187	rhodospirillum
5367	6	0	0	8	584	1	AYFA_MERBA	P23187	rhodospirillum
5368	6	0	0	8	584	1	AYFA_MERBA	P23187	rhodospirillum
5369	6	0	0	8	584	1	AYFA_MERBA	P23187	rhodospirillum
5370	6	0	0	8	584	1	AYFA_MERBA	P23187	rhodospirillum





777	0	0.8	114.1	MEM2-DHORE	P55163	CANONONAB
778	6	0.8	114.5	MEM2-DHORE	G99411	DIOSPOPHAB
779	6	0.8	115.0	C9EA-BACXA	Q96114	BEACILLUS
780	6	0.8	115.0	C9EA-BACXA	Q96114	BEACILLUS
781	6	0.8	115.5	C1IB-BACXA	Q45718	BEACILLUS
782	6	0.8	115.7	C8BA-BACXC	Q45703	BEACILLUS
783	6	0.8	115.7	C9CA-BACXC	Q45703	BEACILLUS
784	6	0.8	115.7	C9CA-BACXC	Q45703	BEACILLUS
785	6	0.8	116.0	C1DB-BACXC	Q45747	BEACILLUS
786	6	0.8	116.4	YAV1-XANCV	P44727	XANTHOMONAS
787	6	0.8	116.5	C1DA-BACXA	P19413	BEACILLUS
788	6	0.8	116.5	C1DA-BACXC	P19413	BEACILLUS
789	6	0.8	116.9	C1CB-BACXC	Q45718	BEACILLUS
790	6	0.8	116.9	C1CB-BACXC	Q66377	BEACILLUS
791	6	0.8	116.9	C1CB-BACXC	Q92466	BEACILLUS
792	6	0.8	116.9	EGPA-BACXC	Q92466	BEACILLUS
793	6	0.8	116.9	EGPA-BACXC	Q92466	BEACILLUS
794	6	0.8	117.0	C1CB-BACXC	Q45718	BEACILLUS
795	6	0.8	117.1	TSR1-MOUSE	P35444	MUS MUSCULUS
796	6	0.8	117.1	C1BA-BACXC	Q92416	BEACILLUS
797	6	0.8	117.1	C1BA-BACXC	Q92416	BEACILLUS
798	6	0.8	117.4	C1EB-BACXA	P03746	BEACILLUS
799	6	0.8	117.4	C1EB-BACXA	P03746	BEACILLUS
800	6	0.8	117.6	C1IA-BACXC	P02865	BEACILLUS
801	6	0.8	117.6	C1CB-BACXA	P56533	BEACILLUS
802	6	0.8	117.8	C1XC-BACXC	P05068	BEACILLUS
803	6	0.8	117.8	C1XC-BACXC	P17442	BEACILLUS
804	6	0.8	117.8	PHB1-YEAST	P17442	BEACILLUS
805	6	0.8	118.1	C1AD-BACXA	Q10744	BEACILLUS
806	6	0.8	118.1	C1AD-BACXA	Q10744	BEACILLUS
807	6	0.8	118.1	YV02-METJA	Q60301	METHYLOBAC
808	6	0.8	118.4	CNEE-EMERI	Q00704	EMERICELLA
809	6	0.8	118.8	YKCS-YEAST	P13594	BEACILLUS
810	6	0.8	118.8	YKCS-YEAST	P13594	BEACILLUS
811	6	0.8	119.0	YK01-SOHO	Q11798	OLIVOSARMA
812	6	0.8	121.0	EGFR-HUMAN	P00513	HOMO SAPIENS
813	6	0.8	121.0	EGFR-MOUSE	Q01279	MUS MUSCULUS
814	6	0.8	122.5	B1A-BACXC	P23138	CATTUS FELIS
815	6	0.8	122.7	C1CB-BACXC	P05517	BEACILLUS
816	6	0.8	122.8	C1BA-BACXC	P05517	BEACILLUS
817	6	0.8	122.8	C1BA-BACXC	P05517	BEACILLUS
818	6	0.8	122.8	C1CB-BACXC	P05517	BEACILLUS
819	6	0.8	122.8	C1CB-BACXC	P05517	BEACILLUS
820	6	0.8	123.3	C1BC-BACXC	P05517	BEACILLUS
821	6	0.8	123.3	C1BC-BACXC	P05517	BEACILLUS
822	6	0.8	124.4	Y107-BACXC	P79312	HYPOGLOSSUS
823	6	0.8	127.5	YA09-SOHO	Q10164	OLIVOSARMA
825	6	0.8	128.6	YKFS-YEAST	P28273	BEACILLUS
826	6	0.8	128.7	YV02-HELIPY	Q48485	HELICOBACTER
827	6	0.8	129.0	VAC02-HELIPY	P55961	HELICOBACTER

879	6	0.8	2431	1	POLN_SFV	P0841	seal.iki
880	6	0.8	2437	1	NORC_BRAE	P4650	brachy.arp
881	6	0.8	2440	1	CPRI_BRAE	P4651	brachy.arp
882	6	0.8	2442	1	CPRI_HUMAN	O92733	homo.sap
883	6	0.8	2472	1	SPON_HUMAN	Q19813	homo.sap
884	6	0.8	2479	1	POLN_BHAV	P19897	rosm.rap
885	6	0.8	2480	1	POLN_BHAV	P19898	rosm.rap
886	6	0.8	2492	1	POLN_EEVP	P36328	venuste.1
887	6	0.8	2492	1	POLN_EEVP	P27282	venuste.1
888	6	0.8	2512	1	POLN_SINVO	P03317	sinbiba
889	6	0.8	2514	1	POLN_SINVO	P37285	sinbiba
890	6	0.8	2531	1	POLN_SINVO	O07008	reticul.n
891	6	0.8	2550	1	PEPS2_BACU	P19846	baellu.uss
892	6	0.8	2550	1	PEPS2_BACU	O05057	stairlip
893	6	0.8	3093	1	POLG_EEVP1	O65730	b genome
894	6	0.8	3175	1	RPOA_EEVP	P19811	equine.a
895	6	0.8	3183	1	POC7_CEREI	P03156	canorhina.a
896	6	0.8	3443	1	POC7_CEREI	P19891	y genome
897	6	0.8	3443	1	POLG_VEFY2	P19891	y genome
898	6	0.8	3587	1	SRN1_BACU9	P27206	baellu.uss
899	6	0.8	3587	1	SRN1_BACU9	O61001	mus.mus
900	6	0.8	3635	1	LAM5_MOUSE	O04561	lelystad.a
901	6	0.8	3659	1	RPOA_LELV	O04561	lelystad.a
902	6	0.8	3866	1	IRRX_MOUSE	P55200	mus.mus
903	6	0.8	4639	1	DYRC_MOUSE	P17276	dmochoph.c
904	6	0.8					
905	6	0.8					

828	6	0	8	1291	1	VACV_HELP	Q4828	helioscap
829	6	0	8	1292	1	RNCV_MICE	Q4829	hypocleas
830	6	0	8	1293	1	PCSV_MICE	P15524	hypocleas
831	6	0	8	1296	1	VACV_HELP	Q48247	helioscap
832	6	0	8	1310	1	VACV_HELP	Q48247	helioscap
833	6	0	8	1322	1	SOS_DROME	P22235	dirosophia
834	6	0	8	1327	1	PCSV_MICE	P22235	dirosophia
835	6	0	8	1337	1	RISC_ECOLI	P16918	escherichia
836	6	0	8	1408	1	CEAL_YEAST	P47102	asaccharo
837	6	0	8	1409	1	HAPV_YEAST	P44596	hemophilus
838	6	0	8	1411	1	YB63_CAEEL	P13342	asaccharo
839	6	0	8	1412	1	YB63_CAEEL	P13342	asaccharo
840	6	0	8	1432	1	YB63_YEAST	P17883	asaccharo
841	6	0	8	1443	1	REST_CHICK	Q42184	gallus
842	6	0	8	1444	1	CESV_BOVIN	P13342	asaccharo
843	6	0	8	1451	1	PCSV_MICE	Q10569	bos taurus
844	6	0	8	1451	1	DPOK_BAT	Q09042	retus
845	6	0	8	1453	1	VY73_BOVIN	Q09043	bos taurus
846	6	0	8	1456	1	RHPO_PAXI	P17773	potamo
847	6	0	8	1461	1	RHPO_PAXI	P17773	potamo
848	6	0	8	1481	1	RNCV_MICE	P45468	dentostom
849	6	0	8	1508	1	ATPS_MOUSE	Q54867	mus mus
850	6	0	8	1508	1	ATPS_MOUSE	Q54867	mus mus
851	6	0	8	1520	1	PCSV_MICE	Q26570	mus mus
852	6	0	8	1522	1	PCSV_MICE	Q26570	mus mus
853	6	0	8	1538	1	PEPB_MCTD	Q10978	escherich
854	6	0	8	1552	1	YF2A_CHICK	Q43130	gallus
855	6	0	8	1584	1	PCSV_MICE	Q10978	escherich
856	6	0	8	1584	1	PCSV_MICE	Q10978	escherich
857	6	0	8	1595	1	SOS_DROME	Q10978	escherich
858	6	0	8	1613	1	VY73_CAEEL	P26765	asaccharo
859	6	0	8	1616	1	VY73_CAEEL	P26765	asaccharo
860	6	0	8	1616	1	VY73_CAEEL	P26765	asaccharo
861	6	0	8	1706	1	CTAA_DROME	P15318	bordestia
862	6	0	8	1746	1	TENA_PIC	Q39316	mus mus
863	6	0	8	1818	1	HNMY_PCEPA	P27471	mycoplasma
864	6	0	8	2032	1	PCSV_MICE	Q10008	hom sapi
865	6	0	8	2032	1	PCSV_MICE	Q10008	hom sapi
866	6	0	8	2051	1	FAS1_YEAST	P07149	a fatty
867	6	0	8	2139	1	PCSV_MOUSE	Q10185	mus mus
868	6	0	8	2153	1	PCSV_MOUSE	Q10185	mus mus
869	6	0	8	2153	1	PCSV_MOUSE	Q10185	mus mus
870	6	0	8	2169	1	CCNC_BAT	P23202	retus
871	6	0	8	2171	1	CCNC_BAT	P13381	oryzotola
872	6	0	8	2199	1	GLNE_MESA	Q10560	medicago
873	6	0	8	2231	1	DISE_YEAST	P13381	oryzotola
874	6	0	8	2232	1	DISE_YEAST	P13381	oryzotola
875	6	0	8	2244	1	PRGL_SCIPO	Q09794	schistos
876	6	0	8	2249	1	PCSV_MICE	P15921	richestia
877	6	0	8	2249	1	PCSV_MICE	P15921	richestia
878	6	0	8	2416	1	SCOV_HUMAN	P02549	hom sapi

879	6	0.8	2431	1	POLK.SPV	P08411 semliki for
880	6	0.8	2437	1	NPCT_SHAKE	P46530 brachyotio
881	6	0.8	2438	1	NPCT_SHAKE	P46530 brachyotio
882	6	0.8	2442	1	CBP_HUMAN	O02793 homo sapien
883	6	0.8	2452	1	SPCK_HUMAN	Q13813 homo sapien
884	6	0.8	2459	1	POLK.BVNV	P13813 rovea sierr
885	6	0.8	2463	1	NPCT_SHAKE	P13813 rovea sierr
886	6	0.8	2492	1	POLK.EEVP	P37282 venezuelan
887	6	0.8	2492	1	POLK.EEVP	P37282 venezuelan
888	6	0.8	2512	1	POLK.SINOV	P03312 alindiba vir
889	6	0.8	2512	1	POLK.SINOV	P03312 alindiba vir
890	6	0.8	2514	1	POLK.SINOV	P37283 modified vit
891	6	0.8	2531	1	NPCT_RAT	Q07608 ratluna novy
892	6	0.8	2550	1	PPST_BACST	P19246 bacillus au
893	6	0.8	2550	1	PPST_BACST	P19246 bacillus au
894	6	0.8	1027	1	POLG.PEYVI	Q05057 paratub yel
895	6	0.8	1093	1	POLG.BEYVI	Q65736 b genome po
896	6	0.8	3175	1	RPOA.EAVI	P13811 equine acro
897	6	0.8	3175	1	RPOA.EAVI	P13811 equine acro
898	6	0.8	3411	1	POLG.YEYVI	P03314 y genome po
899	6	0.8	3411	1	POLG.YEYVI	P19206 bacillus au
900	6	0.8	3587	1	SPST_BACST	P27206 bacillus au
901	6	0.8	3587	1	SPST_BACST	P27206 bacillus au
902	6	0.8	3113	1	LMA.DROSE	Q04012 dirosophila
903	6	0.8	3859	1	RPOA.LEYVI	Q04507 leytelad vi
904	6	0.8	3859	1	HRX.MOUSE	P53200 mus musculu
905	6	0.8	4639	1	DTIC.DROSE	P37296 drosophila

RESULT 1

PSBL\_HUMAN

STANDARD:

PRT: 750 AA.

ALIGNMENTS

Accession

Species

Standard

PRT

750 AA.

Alignments

879

6

0.8

2431

1

POLK.SPV

P08411 semliki for

880

6

0.8

2437

1

NPCT\_SHAKE

P46530 brachyotio

881

6

0.8

2438

1

NPCT\_SHAKE

P46530 brachyotio

882

6

0.8

2442

1

CBP\_HUMAN

O02793 homo sapien

883

6

0.8

2452

1

SPCK\_HUMAN

Q13813 homo sapien

884

6

0.8

2459

1

POLK.BVNV

P13813 rovea sierr

885

6

0.8

2463

1

NPCT\_SHAKE

P13813 rovea sierr

886

6

0.8

2492

1

POLK.EEVP

P37282 venezuelan

887

6

0.8

2492

1

POLK.EEVP

P37282 venezuelan

888

6

0.8

2512

1

POLK.SINOV

P03312 alindiba vir

889

6

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2512

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POLK.SINOV

P03312 alindiba vir

890

6

0.8

2514

1

POLK.SINOV

P37283 modified vit

891

6

0.8

2531

1

NPCT\_RAT

Q07608 ratluna novy

892

6

0.8

2550

1

PPST\_BACST

P19246 bacillus au

893

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0.8

2550

1

PPST\_BACST

P19246 bacillus au

894

6

0.8

1027

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POLG.PEYVI

Q05057 paratub yel

895

6

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1093

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POLG.BEYVI

Q65736 b genome po

896

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0.8

3175

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RPOA.EAVI

P13811 equine acro

897

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3175

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RPOA.EAVI

P13811 equine acro

898

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0.8

3411

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POLG.YEYVI

P03314 y genome po

899

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3411

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POLG.YEYVI

P19206 bacillus au

900

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0.8

3587

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SPST\_BACST

P27206 bacillus au

901

6

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3587

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SPST\_BACST

P27206 bacillus au

902

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LMA.DROSE

Q04012 dirosophila

903

6

0.8

3859

1

RPOA.LEYVI

Q04507 leytelad vi

904

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0.8

3859

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HRX.MOUSE

P53200 mus musculu

905

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4639

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DTIC.DROSE

P37296 drosophila

FUNCTION: MAY INTERACT WITH TRANSDUCIN OR ANOTHER LIGAND AND

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RA	MEDLINE:95-203286. PubMed:7895733.
RK	Gargela U.F., Pucher B.C., Kobayashi B., Latier G.I., Schwender B.,
RT	"Protein identifications for a Saccharomyces cerevisiae protein
RF	database."
RL	J. Proteome Res. 15:1466-1466(1994).
RP	SEQUENCE OF 27-35 AND 134-145
RR	SFRAIIN=ATCC 14827 / SROQJ:
RK	MEDLINE:95190729; PubMed:9038161;
RT	Nucleotide and amino acid sequence changes associated with growth of
RF	Saccharomyces cerevisiae in 1,4 M NaCl. Evidence for osmotic
RR	induction of glycerol dissimilation via the dihydroxyacetone
RM	pathway. Chem. 272:5544-5554(1997).
RN	(5)
RA	ACETYLATION.
RK	Gargela U.F., Pucher B.C., Kobayashi B., Latier C.I., Schwender B.,
RT	Submitted (SEP-1994) to the SWISS-PROT data bank.
CC	- FUNCTION BINDS DNA. REQUIRED FOR THE ASSEMBLY AND/OR STABILITY OF
CC	- THE 40S RIBOSOMAL SUBUNIT
CC	- TWO GENES FOR 50 S IN YEAST
CC	- SIMILARITY: BELONGS TO THE SLP FAMILY OF RIBOSOMAL PROTEINS.
CC	- THIS SWISS-PROT entry is copy-righted. It is produced through a collaboration
CC	between the European Bioinformatics Institute and the Swiss Institute of
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (see <a href="http://www.lsb.slb.ch/announcements/">http://www.lsb.slb.ch/announcements/</a> )
CC	EMBL: M88277 LAB05643.1 ;
DR	EMBL: Z72899 LAB97241.1 ;
DR	EMBL: X72899 LAB97241.1 ;
DR	SISS-20PACC: P32905; YEA5T.
DR	YEPD: 93927 ;
DR	SDS: S0003446; RESOA.
DR	PVAL: PRO0318; Ribosomal_32.1.
DR	PRITE: PR00365; RIBOSOMAL_S2.1 ;
DR	PRITE: PR00362; RIBOSOMAL_S2.1 ;
DR	RIBOSOMAL_POSESIT: DNA-binding; Acetylation; Multisene family.
FT	INTL_JEN 0
FT	MDL_RES 1 ACETYLATION
SO	SEQUENCE 251 AA: 27893 MW: 489263515082C75A CMCA4:

```
CC      DBL; U3756; AAC9226.1;
CC      DR PHBL; Z72200; CAA92578.1;
CC      DR YEPD; 9268;
CC      DR SGD; S0004038; RPS0B;
CC      DR TRPMDPOD; PRO01465;
CC      DR TRPMDPOD; PRO01465; RIBOSOMAL_S2_1;
CC      DR PRINTS; PR00395; RIBOSOMAL_S2;
CC      DR PROSITE; PS00962; RIBOSOMAL_S2_1;
CC      DR PROSITE; PS00962; RIBOSOMAL_S2_1;
CC      DR PROSITE; PS00962; RIBOSOMAL_S2_1;
CC      DR INTRES; protdin; DDB BINDING BY SIMILARITY; Multisense family;
CC      FT MOD_RES 251 AA ACETYLATION (BY SIMILARITY);
CC      SEQUENCE 251 AA; 27831 MW; 20B7DE90A5FEAF8 CRC64;
```

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Query Match          1.0%; Score 7; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 388 TERNSEN 354
Db 239 TERNAEN 245
```

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RESULT 14
ID RS3A.SCHRO STANDARD: PRT: 251 AA.
CC 01-NOV-1995 (Rel. 32, Created)
CC 01-NOV-1995 (Rel. 32, Last sequence update)
CC 10-MAY-2000 (Rel. 39, Last annotation update)
CC 40S RIBOSOMAL PROTEIN S2AC-N (91-A).
CC 01-NOV-1995 (Rel. 32, Created)
CC Schizosaccharomyces pombe (Fission yeast);
CC Baktayola; Funtii; Acetomycola; Schizosaccharomycetales;
CC Schizosaccharomycetales; Schizosaccharomycetes
CC SOURCE FROM N.A.
```

```
RP STRAIN=972;
RA Orell C.; Bowen S.; Barrel B.C.; Rajadream M.A.; Watan S.V.;
RA Schizosaccharomycetes; THERE ARE TWO GENES FOR S1 IN S.POME;
CC -1- SIMILARITY: BELONGS TO THE SAME FAMILY OF RIBOSOMAL PROTEINS.
```

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01 Nov 99 9 11:14:15 2001
us-08-403:803-3-coyp_45_750-0119.rsp

Query Match 1.00; Score 7.09.1; Length 251;
Matched 17; Conservative 0%; PctIdent 100.00;
0Y 388 TMSKRN 394
01 | | | | |
DB 239 TMSKRN 245

RESULT 13
RESIDUE YEAR STANDARD PRT 251 AA.
AC 196654
DT 01-NOV-1995 (rel. 32, Cited)
DT 01-NOV-1995 (rel. 32, Last sequence update)
DT 15-DEC-1998 (rel. 37, Last annotated sequence)
CC NDBS OR NMAS OR NMA OR Y572 OR Y570A8R OR L2118
CC Saccharomyces cerevisiae (Baker's yeast).
CC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
CC Saccharomycetaceae; Saccharomycas.
RP SEQUENCE FROM N.A.
RA Demariova M.V., Formosa T.G., Ellis S.R.;
RL Submitted (JUG-1995) to the EMBL/GenBank/DBJ databases.
RA Andre B., Ureziereau L.A.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RA [1]
RA [2]
RA [3]
RA SEQUENCE OF 52-55, 101-110 AND 134-145.
RA [1]
RA [2]
RA [3]
RA MEDLINE=97190279; PubMed=6028161;
RA Norbeck J., Blomberg A.;
RA "Metabolic and regulatory changes associated with growth of
RA Saccharomyces cerevisiae in 1,4-NaHCO3 and glycerol
RA medium of glycerol dissimilation in the dihydroxyacetone
RA pathway".
RL J. Biol. Chem. 272:5544-5554(1997).
CC -1- THE 408 RIBOSOMAL PROTEIN TWO GENES FOR SO IN YEAST.
CC -1- SIMILARITY BELONGS TO THE 52P FAMILY OF RIBOSOMAL PROTEINS.
CC
CC THIS SWISS-PROT entry is copy-right. It is produced through a collaboration
CC between the EMBL, the EMBL/GenBank/DBJ databases and the Swiss Institute
CC of Bioinformatics. There are no restrictions on its use. It may be
CC used by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by, and for commercial
CC entities requires a license agreement (see http://www.lab.slb.ch/announce
CC or send an email to license@slb.slb.ch).

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CC entitled requires a license agreement (see http://www.lsb-std.ch/announce/
CC or send an email to a license@lsb-std.ch).
CC
CC PDB: 1E4108; CAS:1095; 1.
CC INTERNO: IPRO01593; 1.
CC
CC PRM: PEO1015; Ribosomal_SAB: 1
CC PROSTR: P50119; Ribosomal_SAB: 1
CC PROSTR: P50119; Ribosomal_SAB: 1
CC PROSTR: P50119; Ribosomal_SAB: 1
CC INT_KE2: 0
CC INT_KE2: 0
CC SEQUENCE: 251 AA; 2A25A6345A9B98 CMC64;

Query March 1.0% score 7; db 1
Best local similarity: 100.0%; Pval: No 32;
Matches 1; Conservative 0; Mismatches
DB 223 DANKLE 229

QY 257 DANKLE 263
|||||||
DB 223 DANKLE 229

RESULT 15
NDPM,CHICK STANDARD: PRT: 310 AA.
AC 5/9/1986:2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DI 01-OCT-2000 (Rel. 40, Last annotation update)
DE NEUROGENIC DIFFERENTIATION FACTOR NEURON.
CC Eukaryotic Metazoa: Chordata; Crataea; Vertebrata; Euteleostomi;
CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianine;
CC Gallus.
CC
CC RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN; TISSUE=SEPTIMA.
RX MEDLINE=9744246; Epub=9731021; Alied C., Ballivet M.,
RA Matic U.; Matic-Sabzkanaki L., Alied C., Ballivet M.,
RT "Neurot a neural helix-loop-helix transcription factor, defines a
RT new translaton stage in neurogenesis."
CC DEVELOPMENT. ACTS AS A DIFFERENTIATION FACTOR DURING NEUROGENESIS.
CC TRANSCRIPTIONAL ACTIVATOR. BINDS DNA ON E-BOX CONSENSUS SEQUENCE
CC 5'-CANNNG-3'.
CC
CC -1- SUBUNIT EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
CC -1- SUBUNITAL LOCATION: NUCLEAR (POTENTIAL).
CC -1- TISSUE SPECIFICITY: DEVELOPING NERVOUS SYSTEM.
CC -1- DEVELOPMENTAL STAGE: EXPRESSION IN THE DENDROGENIC NERVOUS SYSTEM
CC IS TRANSIENT AND RESTRICTED TO CELLS LINKING THE VENTRICULAR ZONE

```









Query Match 1.00; Score 7; DB 1; Length 470  
Best Local Similarity 100.00; Pred. No. 55;

CATA_HUMAN	STANDARD;	PRT;	526 AA
ID CATA_HUMAN			
1000000000			

D7 01-0C9-2000 (Ref. 10). Last sequence update)

D8 01-0C9-2000 (Ref. 10). Last annotation update)

D9 CMTVLA5E (ec 1.11.1.6).

DB Homo sapiens (Human).

DC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi

DD Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

RE [1] SOURCE FROM N.A.

RN TISSUE=KIDNEY;

RC MEDLINE=68286565; PubMed=3755526;

RA Ball G., Najjarin R.C., Mullenbach G.T., Hallowell J.R.A.;

RT "cDNA sequence coding for human kidney catalsae";

RL Nucleic Acids Res. 14:5561-5562(1986).

RZ [2]

RP SEQUENCE FROM N.A.

RQ MEDLINE=68286564; PubMed=3755525;

RA Quan P.F., Korneluk R.G., Tropak B.B., Gravel R.A.;

RT "Cloning and characterization of the human catalsae gene";

RL Nucleic Acids Res. 14:5531-5535(1986).

RZ [3]

RP SEQUENCE OF 76-526 FROM N.A.

RQ MEDLINE=65058457; PubMed=6549744;

RA Korneluk R.C., Quan P., Letat H.B., Guise K.S., Willard H.F.,

RT Holmes M.T., Gravel R.A.

RT "Isolation of human fibroblast catalsae cDNA clone. Sequence o

RL J Biol. Chem. 259:13819-13823(1984).

RZ [4]

RP SEQUENCE OF 1-21 FROM N.A.

RQ MEDLINE=94110731; PubMed=6839800;

RA Isomarchand P., Crystal R.G.;

RT "Vulnerability of the human airway epithallium to hyperoxia.

RT Constitutive expression of the catalsae gene in human bronchial

RT epithelial cells despite oxidant stress";

RL J. Clin. Invest. 93:297-302(1994).

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CC -I- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O
CC -I- COPACTOR: HEME GROUP AND NADP.
CC -I- SUBUNIT: HOMOTETRAMER.
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CC - - DISEASE DEFICIENCY IN CAT CAUSES ACNTASTIA.
CC - - SIMILARITY BELONGS TO THE CANINAE FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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RT   analysis of cDNA clones from human cell line Kc-1.
CC   Genbank accession: J12251-2251934).
CC   This Swiss-Prote entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation at
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CC   entities requires a license agreement (see http://www.emb-nib.ch/announce/
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DB 740 RDYAVVL 746
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DT 01-MAR-1994 (Rel. 28; Last annotation update)
DT 01-SEP-1994 (Rel. 28; Last protein update)
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CD Saccharomyces cerevisiae (Baker's yeast).
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OC Saccharomycetaceae; Ascomycota; Saccharomycetes.
NC 11
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RP MEDLINE:95104817; PubMed-7785314;
RP Medges P. E., Jackson S.P., Brown L.D., Beggs J.D.
RP Yeast 11:37-342(1995).
RP The P88 is a conserved factor of the P88 splicing factor *.
RN (2)
RS SEQUENCE FROM N. A.
RS PubMed-67838907; PubMed-67838907;
RS Shes J.E., Roy J.H., Johnston L.H.;
RS The budding yeast US ANBP P88 is a highly conserved protein which
RS links RNA splicing with cell cycle progression.
RS Nucleic Acids Res. 21:3555-3564(1994).

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RX	du Z., Esvellio A., Fulton L,
RA	Lattelle P., Louis E.J., M
RA	Nhan M., Rifkin L., Riles L,
RA	Vignati D., Wilcox L., Monle
RT	"Complete nucleotide sequence
RT	VIII."
RL	Science 265:2077-2082(1994).
RL	CLACETARYON.
RL	Jackson S.P., Lossky M., See
RX	MEDLINE=88225580; PubMed=85
RX	Cloning of the RNase gene of
RT	the yeast <i>Saccharomyces cere</i>
RT	pre-mRNA splicing." demonst
RL	Mol. Cell Biol. 8:1057-1075
CC	- PROMOTER INVOLVED IN PR
CC	IN CELL CYCLE BINDS ENRICH
CC	- SUBCELLULAR LOCATION: N
CC	- SIMILARITY: STRONG, TO
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DB	EMBL: U00927; AA857044.1 -
DB	PIR: S34670; S34670.
DB	PIR: S34670; S34670.
DR	mRNA processing; mRNA aplice
NM	mRNA-binding.
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FT	DOMAIN 4 72
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Catalytic; Catalysis; Zinc-finger;
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RT crystallographic unit cell.
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RT BiochemJ 363:1-56(1986)
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CC THE FAVORABLE DEPTH FOR GROWTH. GVA TYPE PROTEINS FORM THE
CC 1- SUBCELLULAR LOCATION: GAS VESICLE MEMBRANE.
CC 1- SIMILARITY: TO OTHER GAS VESICLE PROTEINS TYPE A.
CC
CC The following entry is a copy of an entry produced through a computer
CC search of the SwissProt database for the keyword "gas vesicle".
CC The European Bioinformatics Institute. There are no restrictions on
CC use. By non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC or send an email to 1bcses@db.stb.ch)
CC
CC EMBL: M3260; AA88487.1;
CC EMBL: U11099; AAAS8708.1;
CC EMBL: U11099; AAAS8708.1;
CC PIR: A23851; SVFE.
CC
CC INTERPRO:IPR000638;
CC PROSITE: P00234; GAS_VESICLE_A.1;
CC PROSITE: P00669; GAS_VESICLE_A.2; 1.
CC GAS VESICLE. 0
CC
CC FT CONFLICT 37 37 E -> Q (IN REF. 3).
CC FT CONFLICT 67 70 AVFA -> VPAA (IN REF. 3).
CC SEQUENCE 70 AA: 7397 MW: 786233377651A5CF C6K64;
CC
CC Query Match 0.83; Score 6; DB 1; Length 70;
CC Best Local Similarity 100.0%; Pred. No. 1;le=0.2;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0
CC
CC QY 240 AENVGL 345
CC Db 57 AENVGL 62
CC
CC RESULT 49
CC GVA_PRED1
CC GVA_PRED1 STANDARD; PART 70 AA.

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CC      -1- SIMILARITY TO OTHER GAS VESICLE PROTEINS TYPE A.
CC
OC
DR      EMBL: X06085 CMA2467.1 ;
DR      EMBL: M16731 AAA24884.1 ;
DR      PIR: B29851 SVXC ;
DR      PIR: A27415 AATV5 ;
DR      DDBJ: F000433 GAS_VESICLE_1 ;
DR      PAM: P00741 GAS_VESICLE_A.1 ;
DR      PROSITE: PS00344 GAS_VESICLE_A.1 ;
DR      PROSITE: PS00669 GAS_VESICLE_A.2 ;
FM      GAS_VESICLE_0
FM      VARIANT 26 0
FM      SEQUENCE 70 AA: 7283 NW: 19125337678BD0 CRC64:
SQ
Query Match          0 R% Score 6; DB 1; Length 70;
Beat Local Similarity 100.0%; Pred. No. 1;e+02;
Matches    6; Conservative    0; Mismatches     0; Indels    0; Gaps    0
GY      240 AENVGL 245
DB      57 AEAVGL 62

RESULT: 50
GVPV_MICB
ID      GVPV_MICB   STANDARD:      PRT:       70 AA.
AC      P06812: 1988 [Prl] 10. Created)
MC      1-MAB-1988 (Ref. 10. Gas sequence update)
DT      01-MAY-1988 (Ref. 10. Gas sequence update)
DT      01-APR-1990 (Ref. 14. Last annotation update)
DE      GAS VESICLE PROTEIN (GVP).
OS      GVPV.
NC      Bacillus subtilis sp. (strain NC 84/11)
OC      Bacteria; Cyanobacteria; Chromococcales; Microcystis.
[ ]
SEQUENCE: 071563; PubMed:008934;
RP      MEDLINE: D-8 Malhotra et al., J. Biol. Chem. 263:1117-1121 (1988);
RA      Kary & Malhotra, J. Biol. Chem. 263:1117-1121 (1988);
RT      "Complete amino acid sequence of cyanobacterial gas-vesicle protein
BT      indicates a 70-residue molecule that corresponds in size to the
CC      crystallographic unit cell."
CC      Location: cytoplasmic
CC      FUNCTION: GAS VESICLES ARE SMALL, HOLLOW, GAS FILLED PROTEIN
CC      MICROCAPSULES THAT ALLOW THE POSITIONING OF THE BACTERIA, AT
CC      THE FAVORABLE DEPTH FOR GROWTH. GVA TYPE PROTEINS FORM THE
CC      EXTERIOR SURFACE OF THE CAPSULE MEMBRANE.
CC      -1- SUPERFICIAL LOCATION: GAS VESICLE MEMBRANE.
CC
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AC P07060: 01-APR-1988 (Rel. 07, Created)  
 DT 01-APR-1988 (Rel. 07, Sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last annotation update)  
 DE GAS VESICLE PROTEIN (GVP).  
 GN GVA AND (GVPB OR GVPA2).  
 OS Bacteria: Cyanobacteria: Nostocales: PCC 7601)  
 RN [1]  
 RS SEQUENCE FROM N.A. (GVPB).  
 RX MEDLINE=60441911. PubMed=3997744.  
 RT Molecular cloning and nucleotide sequence of a developmentally  
 RT regulated gene from the cyanobacterium *Calothrix PCC 7601*: a gas  
 RT vesicle protein gene. *J. Cell. Physiol.* 152:661-669 (1992).  
 RL Mediat. Acids Res. 13:1723-1726(1995).  
 RN [2]  
 RS SEQUENCE FROM N.A. (GVPB/GVPA2).  
 RX MEDLINE=92777436. PubMed=3113941.  
 RT Cloning and characterization of the *gvpA* gene from the  
 RT cyanobacterium *Calothrix PCC 7601*.  
 RL Gene 54:83-92(1997).  
 RN [3]  
 RS A developmentally regulated *gvpA* operon is involved in the  
 RT formation of gas vesicles in the cyanobacterium *Calothrix 7601*.  
 RL J. Cell Biol. 137:111-121(1997).  
 RN [4]  
 RS SEQUENCE OF 1-56.  
 RX MEDLINE=87075623. PubMed=3098234.  
 RT Amino acid sequence of the gas vesicle protein  
 RT indicates a 70-residue molecule that corresponds in size to the  
 RT crystallographic unit cell.  
 RL Biochem. J. 236:31-35(1986).  
 RN [5]  
 RS FUNCTION: GAS VESICLES ARE SMALL, RIGID, ROLLING GAS FILLED PROTEIN  
 RS MICROCAPSULES THAT ALLOW THE POSITIONING OF THE BACTERIA, AT  
 RS THE FAVORABLE DEPTH FOR GROWTH. GVA TYPE PROTEINS FORM THE  
 RS ESSENTIAL CORE OF THE STRUCTURE.  
 RS -1- MISCELLANEOUS CHEMICAL ANALYSIS OF PURIFIED GVPs FROM DIFFERENT  
 RS ORGANISMS PREDICTED THAT THE GAS VESICLES COULD BE CONSTITUTED OF  
 RS ONLY ONE PROTEIN SPECIES. THERE ARE TWO GENES ENCODING GAS VESICLE  
 RS -1- PROTEINS. TO OTHER GAS VESICLE PROTEINS TYPE A.  
 RN [6]  
 RS This SwissProt entry is copyright. It is produced through a collaboration  
 RS between the Swiss Institute of Bioinformatics and the EMBL outstation  
 RS at the European Molecular Biology Laboratory. The data are available for  
 RS use by non-profit institutions as long as its content is in no way  
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 RS send an email to [license@isb.ac.uk](mailto:license@isb.ac.uk)).

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DR      PRK120503IPR000638; D
DR      D1_HMP907; CAS.VESICLE; 1
DR      PPM: PR00741; GAS.VESICLE; 1
DR      PROSITE: PS00234; GAS.VESICLE_A.1; 1
DR      PROSITE: PS00669; GAS.VESICLE_A.2; 1
DR      GAS.VESICLE; 0
FM      SEQUENCE: 0
SQ      SEQUENCE: 70 AA: 7442 NM: CPFS98657DEPSC CIRC64;

Query Match          0.8%   Score 6:    DB 1, Length 70;
Needle local similarity 1.000E+00; Positives 1e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      240 AENVGL 245
        |||||
DB       57 AENVGL 62

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Search completed: April 6, 2001, 16:59:42  
Job time: 180 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd

OM protein - protein search, using SW model

Run on: April 6, 2001, 16:54:32 ; Search time 22.9 Seconds  
(Without alignments)  
2093 356 Million cell under/reads

Title: US-08-403-003-2\_COPY\_45\_750  
Page: 706

Sequence: 1 SSNEATNITPRKHNKAFDE.....QIYVAFTVQAAETLSEVA 706

Scoring table: OLIGO  
Gapen 60.0 Gapext 60.0

Searched: 195891 negs, 67900655 residues

**Word size :**

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Listing first 10

Post-processing: Listing first 1000 summaries

Database : PIR\_

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2: p1t2:  
3: p1t3:  
4: p1t4:

Pred. No. is the nu

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SUMMARIES

and is derived by analysis of the total score distribution.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	706	100.0	750	2	A56861
2	706	100.0	750	2	A71761
3	1.3	1.3	703	2	A71761
4	1.3	1.3	1306	2	A78911
5	8	1.1	155	2	A14781
6	8	1.1	155	2	A14781
7	8	1.1	256	2	C72261
8	1.1	1.1	260	2	A74854

8	1	751	2	T0154	hypothetical protein
19	8	1369	2	FA153	hypothetical protein
10	1	1069	2	FA153	hypothetical protein
11	8	1377	2	T0088	glucosyltransferase
12	7	1	64	2	C69220
13	7	1	86	2	H75509
14	7	1	102	2	T93580
15	7	1	120	1	R5688F
16	7	1	103	1	R5688F
17	1	133	2	H75623	conserved hypothetical protein
18	7	1	142	1	B01347
19	7	1	150	1	hypothetical protein
20	7	1	173	2	A72655
21	7	1	200	2	570977
22	7	1	10	1	803
23	7	1	10	1	R8459
24	7	1	10	1	R8459
25	7	1	220	2	S63521
26	7	1	237	1	C31319
27	7	1	246	2	H84149
28	7	1	252	1	S64431
29	7	1	252	1	S64431
30	7	1	252	2	T93219
31	7	1	264	2	C72286
32	7	1	268	2	C72286
33	7	1	313	2	T28675
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35	7	1	318	2	H73382
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104	7	1.0	609	2	Y45278	oligopeptide ABC
105	7	1.0	609	2	Y45278	oligopeptide ABC
106	7	1.0	609	2	Y45278	oligopeptide ABC
107	7	1.0	609	2	Y45278	oligopeptide ABC
108	7	1.0	609	2	Y45278	oligopeptide ABC
109	7	1.0	609	2	Y45278	oligopeptide ABC

110	6	0.8	70	1	SVK1	gas vesicle protein
111	6	0.8	70	1	SVK310	gas vesicle protein
112	6	0.8	71	1	SVK1	antigen-binding F
113	6	0.8	71	2	EB151	gas-vesicle protein
114	6	0.8	72	2	EB158	gas vesicle protein
115	6	0.8	72	2	EB158	gas vesicle protein
116	6	0.8	80	2	EB109	hypothetical protein
117	6	0.8	81	2	TC0304	reverse transcriptase
118	6	0.8	83	2	726545	hypothetical protein
119	6	0.8	85	2	459564	hypothetical protein
120	6	0.8	85	2	459564	hypothetical protein
121	6	0.8	86	1	RB0023	hypothetical protein
122	6	0.8	86	1	RB0023	ribosomal protein
123	6	0.8	86	2	A14510	homeotic protein
124	6	0.8	86	2	B54705	hypothetical protein
125	6	0.8	87	2	569490	hypothetical protein
126	6	0.8	87	2	569490	hypothetical protein
127	6	0.8	87	2	500836	hypothetical protein
128	6	0.8	89	1	1PMW41	benzoxazin A-2 precursor
129	6	0.8	89	1	1PMW41	benzoxazin A-2 precursor
130	6	0.8	89	2	569481	benzoxazin A-4 precursor
131	6	0.8	90	1	1PMW31	benzoxazin B-1 precursor
132	6	0.8	90	1	1PMW32	benzoxazin B-2 precursor
133	6	0.8	90	2	569486	benzoxazin B-2 precursor
134	6	0.8	90	2	569486	benzoxazin B-2 precursor
135	6	0.8	90	2	569488	benzoxazin B-7 precursor
136	6	0.8	90	2	569491	benzoxazin B-7 precursor
137	6	0.8	90	2	569492	benzoxazin B-11 precursor
138	6	0.8	90	2	569492	benzoxazin B-11 precursor
139	6	0.8	90	2	500840	benzoxazin D-1 s1
140	6	0.8	91	2	500803	benzoxazin B-1 homo
141	6	0.8	91	2	500905	benzoxazin B-2 homo
142	6	0.8	92	2	569478	benzoxazin A-4 precursor
143	6	0.8	92	2	569482	benzoxazin A-1 precursor
144	6	0.8	92	2	569482	benzoxazin A-1 precursor
145	6	0.8	92	2	569482	benzoxazin A-7 precursor
146	6	0.8	92	2	569479	benzoxazin A-9 precursor
149	6	0.8	92	2	500825	hypothetical protein
150	6	0.8	92	2	D70115	hypothetical protein
151	6	0.8	97	2	507266	hypothetical protein
152	6	0.8	97	2	507266	hypothetical protein
153	6	0.8	100	2	750611	hypothetical protein
154	6	0.8	100	2	750611	hypothetical protein
155	6	0.8	106	2	529465	chlorophyll CP10
156	6	0.8	106	2	A14860	chlorophyll CP10
157	6	0.8	107	2	521207	nitrogen fixation
158	6	0.8	107	2	521207	probable membrane
159	6	0.8	108	2	528262	probable membrane
160	6	0.8	108	2	528262	PTSD1 protein

161	0	0	109	2	A54678	monocyte chemo
162	0	0	110	2	S51149	antibody light chain
163	0	0	111	2	S51149	substance P alpha
164	0	0	112	2	S51149	substance P alpha
165	0	0	113	2	B41871	hypothetical protein
166	0	0	113	2	T42882	hypothetical protein
167	0	0	114	2	T45571	hypothetical protein
168	0	0	114	2	T45571	hypothetical protein
169	0	0	120	2	H25532	hypothetical protein
170	0	0	122	2	T01589	hypothetical protein
171	0	0	124	2	T04536	hypothetical protein
172	0	0	124	2	T04536	hypothetical protein
173	0	0	126	2	T02351	hypothetical protein
174	0	0	126	2	B82853	hypothetical protein
175	0	0	127	2	B90888	hypothetical protein
176	0	0	127	2	B90888	hypothetical protein
177	0	0	128	2	G15270	hypothetical protein
178	0	0	129	2	SPH08	hypothetical protein
179	0	0	129	2	B70891	hypothetical protein
180	0	0	130	2	G12678	hypothetical protein
181	0	0	130	2	G12678	hypothetical protein
182	0	0	130	2	SPH08	hypothetical protein
183	0	0	130	2	S47038	hypothetical protein
184	0	0	130	2	T43372	hypothetical protein
185	0	0	130	2	G10122	hypothetical protein
186	0	0	130	2	G10122	hypothetical protein
187	0	0	131	2	T38924	hypothetical protein
188	0	0	132	2	T37064	hypothetical protein
189	0	0	132	2	G72609	hypothetical protein
190	0	0	132	2	G72609	hypothetical protein
191	0	0	133	2	E72653	hypothetical protein
192	0	0	134	2	E51133	hypothetical protein
193	0	0	135	2	G10816	hypothetical protein
194	0	0	137	2	C61895	hypothetical protein
195	0	0	139	2	T38894	hypothetical protein
196	0	0	140	2	H54411	hypothetical protein
197	0	0	142	2	G72399	hypothetical protein
198	0	0	142	2	G72399	hypothetical protein
199	0	0	143	2	H81077	hypothetical protein
200	0	0	143	2	E82873	hypothetical protein
201	0	0	144	2	E82873	hypothetical protein
202	0	0	145	1	UC0C1	hypothetical protein
203	0	0	145	1	UC0C1	hypothetical protein
204	0	0	145	1	UC0C1	hypothetical protein
205	0	0	145	2	C76674	hypothetical protein
206	0	0	146	2	G71187	hypothetical protein
207	0	0	147	2	G70921	hypothetical protein
208	0	0	147	2	T04061	hypothetical protein
209	0	0	149	2	D05666	nucleoside-diphosphate
210	0	0	149	2	D05666	nucleoside-diphosphate
211	0	0	149	2	G54134	hypothetical protein

213	212	0	0	0	1	138540	glycine reductase
213	213	0	0	0	150	145450	phosphatase
214	214	0	0	0	150	162217	conserved hypox
215	215	0	0	0	151	628464	acetyltransferase
216	216	0	0	0	152	511368	lysin protein - p
217	217	0	0	0	152	143388	hemolysin-like p
218	218	0	0	0	153	682778	phosphatase
219	219	0	0	0	153	744364	hypothetical pro
220	220	0	0	0	153	128655	hypothetical pro
221	221	0	0	0	155	705449	hypothetical pro
222	222	0	0	0	155	264042	enoyl-CoA hydrat
223	223	0	0	0	158	672691	hypothetical pro
224	224	0	0	0	158	147741	hypothetical pro
225	225	0	0	0	159	856594	hypothetical pro
226	226	0	0	0	159	856594	peptide N-acetyl
227	227	0	0	0	160	718780	hypothetical pro
228	228	0	0	0	160	2	hypothetical pro
229	229	0	0	0	161	746010	translation initia
230	230	0	0	0	161	744325	hypothetical pro
231	231	0	0	0	161	744325	hypothetical pro
232	232	0	0	0	162	871093	hypothetical pro
233	233	0	0	0	163	627889	hypothetical pro
234	234	0	0	0	163	627889	hypothetical pro
235	235	0	0	0	164	576084	hypothetical pro
236	236	0	0	0	165	2	probable RNA heli
237	237	0	0	0	166	675216	hypothetical pro
238	238	0	0	0	166	2	hypothetical pro
239	239	0	0	0	167	685077	conserved hypox
240	240	0	0	0	167	164221	cag phosphotransf
241	241	0	0	0	169	654195	cag phosphotransf
242	242	0	0	0	173	841310	cag phosphotransf
243	243	0	0	0	174	671020	phage homolog p
244	244	0	0	0	174	2	hypothetical pro
245	245	0	0	0	174	2	hypothetical pro
246	246	0	0	0	175	146591	interleukin 10 -
247	247	0	0	0	175	2	hypothetical pro
248	248	0	0	0	175	2	hypothetical pro
249	249	0	0	0	175	672666	hypothetical pro
250	250	0	0	0	176	2	hypothetical pro
251	251	0	0	0	176	671333	hypothetical pro
252	252	0	0	0	176	141524	hypothetical pro
253	253	0	0	0	177	708126	phosphoenolpyru
254	254	0	0	0	178	2	phosphoenolpyru
255	255	0	0	0	178	2	phosphoenolpyru
256	256	0	0	0	178	675018	inorganic pyropho
257	257	0	0	0	179	659467	conserved hypox
258	258	0	0	0	179	2	hypothetical pro
259	259	0	0	0	180	711915	hypothetical pro
260	260	0	0	0	180	2	hypothetical pro
261	261	0	0	0	181	147428	hypothetical pro
262	262	0	0	0	181	2	50S ribosomal pr

[illegible]

365	6	0.8	235	2	138440	fl3 ligand - huma
366	6	0.8	236	2	B64781	hypothetical prote
367	6	0.8	237	2	T05973	perlecan homolog p
368	6	0.8	238	2	B64782	perlecan homolog p
369	6	0.8	239	2	B81210	protein site-destru
370	6	0.8	237	2	S26439	hypothetical prote
371	6	0.8	237	2	B81245	hypothetical prote
372	6	0.8	241	2	T25799	hypothetical prote
373	6	0.8	241	2	S26439	hypothetical prote
374	6	0.8	243	2	A53244	leukocyte antigen
375	6	0.8	243	2	A82024	hypothetical prote
376	6	0.8	243	2	C75608	hypothetical prote
377	6	0.8	244	2	B70412	hypothetical prote
378	6	0.8	244	2	B75140	hypothetical prote
379	6	0.8	245	2	B75140	transcription regu
380	6	0.8	245	2	G43293	hypothetical prote
381	6	0.8	246	2	A71264	hypothetical prote
382	6	0.8	248	2	C69486	RNA methylase hom
383	6	0.8	248	2	F69198	conserved hypotet
384	6	0.8	248	2	F58222	hypothetical prote
385	6	0.8	249	2	S58095	N-acetylglutamate
386	6	0.8	250	2	C63397	hypothetical prote
387	6	0.8	250	2	C63397	pyridoxalminolase
388	6	0.8	251	2	F64745	probable hydroxyc
389	6	0.8	251	2	F64745	conserved hypotet
390	6	0.8	251	2	C81803	ribosomal protein
391	6	0.8	252	2	B41819	hypothetical prote
392	6	0.8	252	2	S10282	matting type swich
393	6	0.8	253	1	MMW285	PS protein - fowlp
394	6	0.8	253	1	F70378	erythrocyte band 7
395	6	0.8	254	2	C65086	hypothetical prote
396	6	0.8	254	2	C65086	hypothetical prote
397	6	0.8	255	2	A24254	ecdysone-induced p
398	6	0.8	255	2	F82099	undecaprenyl dipo
399	6	0.8	256	2	B73454	hypothetical prote
400	6	0.8	256	2	B73454	hypothetical prote
401	6	0.8	257	2	H55875	cell division prot
402	6	0.8	257	2	F56118	probable oxidoredu
403	6	0.8	260	2	F64239	Holliday junction
404	6	0.8	260	2	B72134	AAC transporter, A
405	6	0.8	260	2	T47096	hypothetical prote
406	6	0.8	261	2	S44776	C30A5 protein - Ca
407	6	0.8	261	2	S44776	alkaline 5-dehydr
408	6	0.8	262	2	C81384	paraprotein crystal
409	6	0.8	262	2	A21140	conserved hypotet
410	6	0.8	262	2	A81504	conserved hypotet
411	6	0.8	262	2	B72037	c598 hypothetical
412	6	0.8	262	2	B72037	hypothetical prote
413	6	0.8	262	2	B83546	probable transcrip
414	6	0.8	263	2	A64676	alkaline 5-dehydr
415	6	0.8	263	2	A64676	hypothetical prote

416	6	0.8	263	2	T35686	phosphatidyglycer
417	6	0.8	263	2	T35616	hypothetical prote
418	6	0.8	263	2	S64472	hypothetical prote
419	6	0.8	263	2	S64472	hypothetical prote
420	6	0.8	263	2	D81085	conserved hypotet
421	6	0.8	264	2	C70525	hypothetical prote
422	6	0.8	264	2	C70525	hypothetical prote
423	6	0.8	265	2	S48585	hypothetical prote
424	6	0.8	265	2	S48585	hypothetical prote
425	6	0.8	266	2	A11841	alkaline 5-dehydr
426	6	0.8	266	2	T11594	hypothetical prote
427	6	0.8	267	2	C02764	ecdysone-inducible
428	6	0.8	267	2	C02764	cyclin G1 interact
429	6	0.8	267	2	A12353	flagellar basal bo
430	6	0.8	268	2	A10143	hypothetical prote
431	6	0.8	268	2	A10143	hypothetical prote
432	6	0.8	269	2	A10143	hypothetical prote
433	6	0.8	269	2	D81090	probable ATP-bind
434	6	0.8	269	2	D81090	probable ATP-bind
435	6	0.8	269	2	T40677	multidrug resistanc
436	6	0.8	271	2	A10415	hypothetical prote
437	6	0.8	271	2	S64163	hypothetical prote
438	6	0.8	272	2	S64163	hypothetical prote
439	6	0.8	272	2	T09929	hypothetical prote
440	6	0.8	273	1	C70127	gula protein homol
441	6	0.8	273	1	F44550	diacylglycerol kin
442	6	0.8	273	2	S64163	hypothetical prote
443	6	0.8	273	2	G81429	hypothetical prote
444	6	0.8	273	2	D71436	hypothetical prote
445	6	0.8	273	2	T48619	hypothetical prote
446	6	0.8	273	2	S64163	hypothetical prote
447	6	0.8	276	2	D70191	hypothetical prote
448	6	0.8	276	2	D70191	hypothetical prote
449	6	0.8	277	2	G81473	probable short-cha
450	6	0.8	278	1	NIMVVO	nitrogenase (BC 1
451	6	0.8	278	1	S61425	parB family prot
452	6	0.8	278	2	A47090	urease-associated
453	6	0.8	278	2	A47090	transcription regu
454	6	0.8	278	2	A63430	hypothetical prote
455	6	0.8	278	2	G75883	hypothetical prote
456	6	0.8	279	2	H69753	AAC transporter (A
457	6	0.8	279	2	H69753	hypothetical prote
458	6	0.8	279	2	S64007	hypothetical prote
459	6	0.8	280	2	H69228	fumarate hydratase
460	6	0.8	280	2	T44876	hypothetical prote
461	6	0.8	280	2	H69228	hypothetical prote
462	6	0.8	281	2	A37349	chorion protein a3
463	6	0.8	282	2	H82394	plrin-related prot
464	6	0.8	282	2	H82394	hypothetical prote
465	6	0.8	282	2	T26112	hypothetical prote
466	6	0.8	283	2	T26112	hypothetical prote

467	6	0.8	283	2	C31660	calcium channel pr
468	6	0.8	284	2	S72650	otocoumarin nucleot
469	6	0.8	284	2	C64158	hypothetical prote
470	6	0.8	285	2	A41826	probable phenomene
471	6	0.8	285	2	T11513	hypothetical prote
472	6	0.8	285	2	S70810	hypothetical prote
473	6	0.8	285	2	S70810	type IV piliellin V
474	6	0.8	287	2	T31457	proteohelophyllid
475	6	0.8	287	2	F75362	hypothetical prote
476	6	0.8	288	2	C74407	hypothetical prote
477	6	0.8	288	2	C74407	hypothetical prote
478	6	0.8	291	2	B71491	probable geranyl t
479	6	0.8	291	2	B71491	transcription regu
480	6	0.8	292	2	G69763	transcription regu
481	6	0.8	293	2	D74684	hypothetical prote
482	6	0.8	293	2	B83508	GDPGF family prote
483	6	0.8	294	2	B70398	calcium channel pr
484	6	0.8	294	2	A21660	dihydrodipicolinat
485	6	0.8	294	2	C83432	type III secretion
486	6	0.8	294	2	C83432	geranyltransferas
487	6	0.8	294	2	A82257	nitrogenase (BC 1
488	6	0.8	296	1	J02155	hypothetical prote
489	6	0.8	296	1	J02155	hypothetical prote
490	6	0.8	297	2	C61047	hypothetical prote
491	6	0.8	297	2	C61047	hypothetical prote
492	6	0.8	298	2	C41047	exonuclease 5 synth
493	6	0.8	298	2	C41047	hypothetical prote
494	6	0.8	298	2	T11943	hypothetical prote
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498	6	0.8	299	2	C81255	hypothetical prote
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500	6	0.8	299	2	C81255	hypothetical prote
501	6	0.8	300	2	M64050	glucose kinase hom
502	6	0.8	301	2	T45659	RNR-III transcrip
503	6	0.8	301	2	D70471	GTP-binding protei
504	6	0.8	301	2	C05348	glutathione synthet
505	6	0.8	303	2	A11178	hypothetical prote
506	6	0.8	303	2	A11178	hypothetical prote
507	6	0.8	303	2	F81118	probable galactosy
508	6	0.8	303	2	F81118	probable galactosy
509	6	0.8	304	2	T48281	hypothetical prote
510	6	0.8	304	2	T48281	hypothetical prote
511	6	0.8	305	2	T47040	sterol O-acyltrans
512	6	0.8	305	2	S75667	ribosomal protein
513	6	0.8	305	2	A53340	hypothetical prote
514	6	0.8	306	2	A53340	hypothetical prote
515	6	0.8	306	2	B48947	offitox - Lactobaci
516	6	0.8	306	2	B76277	bacitracin transpo
517	6	0.8	306	2	T11682	bactr protein - Bac

518	6	0.8	307	2	D70384	Beta lactamase pre
519	6	0.8	308	2	B69771	AAC transporter (A
520	6	0.8	309	1	S60157	RING finger protei
521	6	0.8	309	1	A57235	RING finger protei
522	6	0.8	310	2	T41776	hypothetical prote
523	6	0.8	310	2	A41776	hypothetical prote
524	6	0.8	310	2	F64311	hypothetical prote
525	6	0.8	311	2	A65008	hypothetical prote
526	6	0.8	311	2	A65008	hypothetical prote
527	6	0.8	311	2	D69249	hypothetical prote
528	6	0.8	312	2	G69803	AAC transporter (A
529	6	0.8	312	2	T29454	conserved hypotet
530	6	0.8	313	1	Q0P8CL	conserved hypotet
531	6	0.8	314	2	S51375	phosphoprotein pho
532	6	0.8	315	2	D81111	hypothetical prote
533	6	0.8	315	2	D81111	hypothetical prote
534	6	0.8	316	1	L0P172	anexin XII - Hydr
535	6	0.8	316	1	G64782	acidic dipeptidase
536	6	0.8	316	1	S21264	hypothetical prote
537	6	0.8	317	2	S21264	hypothetical prote
538	6	0.8	317	2	T27485	hypothetical prote
539	6	0.8	317	2	T36136	probable ABC-type
540	6	0.8	317	2	B83579	hypothetical prote
541	6	0.8	318	2	S51415	carboxyphosphomem
542	6	0.8	318	2	S51415	conserved hypotet
543	6	0.8	318	2	B69026	hypothetical prote
544	6	0.8	318	2	T35151	hypothetical prote
545	6	0.8	319	2	T45980	hypothetical prote
546	6	0.8	319	2	T45980	hypothetical prote
547	6	0.8	319	2	T45980	hypothetical prote
548	6	0.8	319	2	T45980	hypothetical prote
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550	6	0.8	320	2	T45980	hypothetical prote
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554	6	0.8	321	2	T45980	hypothetical prote
555	6	0.8	321	2	T45980	hypothetical prote
556	6	0.8	322	1	S00046	hypothetical prote
557	6	0.8	322	1	S00046	hypothetical prote
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559	6	0.8	322	1	S00046	hypothetical prote
560	6	0.8	322	1	S00046	hypothetical prote
561	6	0.8	322	1		



824	6	0	8	407	7	C69402	translation related
825	6	0	8	407	7	R71212	promoter activity
826	6	0	8	409	2	E57889	hypothetical protein
827	6	0	8	410	1	ZEB94L	E4F1 protein - phase
828	6	0	8	410	2	F50718	hypothetical protein
829	6	0	8	411	2	G20343	hypothetical protein
830	6	0	8	411	2	G20343	conserved hypothetical
831	6	0	8	411	2	K72506	probable tRNA splicing
832	6	0	8	412	2	T16480	hypothetical protein
833	6	0	8	412	2	T46104	hypothetical protein
834	6	0	8	412	2	T46104	hypothetical protein
835	6	0	8	412	2	G02039	Ltsp100-A - human
836	6	0	8	412	2	G02039	Ltsp100-A - human
837	6	0	8	413	2	F55890	plasma protein receptor
838	6	0	8	413	2	T21099	hypothetical protein
839	6	0	8	414	2	F75295	hypothetical protein
840	6	0	8	414	2	F75295	hypothetical protein
841	6	0	8	415	2	D75516	probable acyl-CoA
842	6	0	8	415	2	A81920	glutaryl-tRNA reductase
843	6	0	8	415	2	C11183	glutaryl-tRNA reductase
844	6	0	8	415	2	C11183	glutaryl-tRNA reductase
845	6	0	8	415	2	H64704	ribulose-bisphosphate
846	6	0	8	415	2	S31627	ribulose-bisphosphate
847	6	0	8	415	2	G71162	hypothetical protein
848	6	0	8	415	2	G71162	hypothetical protein
849	6	0	8	415	2	F46462	hypothetical protein
850	6	0	8	416	2	T40872	probable cell wall
851	6	0	8	417	1	S49051	cyclochrome P450 ty
852	6	0	8	417	1	S67366	hypothetical protein
853	6	0	8	417	2	H83370	hydrogen cyanide s
854	6	0	8	417	2	H83370	hydrogen cyanide s
855	6	0	8	418	2	P70940	hypothetical protein
856	6	0	8	419	1	D86280	glycerol-3-phosphat
857	6	0	8	419	1	D86280	glycerol-3-phosphat
858	6	0	8	419	2	A18151	conserved hypothetical
859	6	0	8	420	2	A17972	ferrochelatase (EC
860	6	0	8	421	2	T04153	hypothetical protein
861	6	0	8	421	2	D56881	hypothetical protein
862	6	0	8	422	2	A17033	conserved hypothetical
863	6	0	8	423	2	A17033	isovaleryl-CoA dehyd
864	6	0	8	423	2	S31169	chitinase - fungus
865	6	0	8	424	2	S47131	chitinase (EC 3.2.1
866	6	0	8	425	2	T05678	hypothetical protea
867	6	0	8	425	2	T05678	hypothetical protea
868	6	0	8	425	2	T47599	nucleoid DNA-bindin
869	6	0	8	425	2	T47599	nucleoid DNA-bindin
870	6	0	8	426	2	T39617	hypothetical protein
871	6	0	8	427	2	K15095	udp-glucose dehydro
872	6	0	8	427	2	T05019	hypothetical proteo
873	6	0	8	427	2	E63185	hypothetical prote
874	6	0	8	427	2	T49132	hypothetical prote

[illegible]





A:Status: preliminary  
A:Molecule type: mRNA  
A:Accession: T44854  
A:Cross-references: EMBL:AL10760  
A:Experimental source: clone DKFZ586B1621  
C:Genetics:  
A:Note: DKFZ586B1621.1

Query Match 1.1% Score 8; DB 2; Length 165;  
Best Local Similarity 100.0%; Pred. No. 3.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 LTRMGCS 268  
DB 29 LTRMGCS 36

## RESULT 6

C72261 spermidine/putrescine ABC transporter, permease protein - *Thermotoga maritima* (strain MS88)

A:Accession: C72261  
C:Date: 11-Jun-1999 sequence\_revision 11-Jun-1999 text\_change 21-Jul-2000

C:Species: *Thermotoga maritima*  
R:Giles, R.E.; Clayton, R.A.; Gill, S.R.; Givim, M.L.; Dodson, R.J.; Hall, D.H.; Hickey, E.K.; Peterson, J.D.; Nelson, M.C.; Cretz, M.K.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; Heidelberg, J.; Sutton, G.G.; Fied  
Nucle 399, 323-329, 1999  
A:Title: Evidence for lateral gene transfer between *Archaea* and *Bacteria* from genome sequence of *Thermotoga maritima*.  
A:Reference number: N7200; NCBI:9287316

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-356 <AMB>  
A:Cross-references: DB:AB01791; DB:AB00512; NID:94981939; PDB:1A04448.1; PID:94981939; TIGR:TM1378  
C:Genetics:  
A:Gene: TM1378  
C:Superfamily: spermidine/putrescine transport system permease protein pol1

Query Match 1.1% Score 8; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 5.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 605 RLDPPKS 612  
DB 150 RLDPPKS 157

## RESULT 7

Query Match 1.1% Score 8; DB 2; Length 751;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 WMBEPCL 384  
DB 413 WMBEPCL 420

## RESULT 9

T47503 ribosomal protein P9K21.210 - *Archaeoglobus fulgidus*

A:Accession: T47503  
C:Date: 20-Apr-2000 sequence\_revision 20-Apr-2000 text\_change 20-Apr-2000

C:Species: *Archaeoglobus fulgidus* (strain ATCC 35061)  
R:Jordan, N.; Banger, S.; Wiedemann, R.; Voss, H.; Unold, M.; Meves, H.W.; Lemcke, K.; Mayer, K.F.X.; Queller, F.; Salan  
A:Reference number: 22467  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1202 <MON>  
A:Cross-references: EMBL:U118657  
A:Experimental source: Cellvax Columbia: BAC clone P9K21

C:Genetics:  
A:Gene: P9K21.210  
A:Note: P9K21.210

Query Match 1.1% Score 8; DB 2; Length 989;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 RNCIDAV 243  
DB 545 RNCIDAV 552

## RESULT 10

A48731 ribonuclease P (BC 3.1.26.5) precursor, mitochondrial - yeast (*Saccharomyces cerevisiae*)

A:Accession: A48731  
C:Date: 21-Jun-2000 sequence\_revision 19-May-1995 text\_change 21-Jul-2000

C:Species: *Saccharomyces cerevisiae*  
R:Dang, Y.L.; Martin, N.C.  
A:Reference number: 561340; 561339; 510802  
J. Biol. Chem. 268, 19791-19796, 1993  
A:Title: Yeast mitochondrial RNase P. Sequence of the RNase P gene and demonstration that its product is a protein subunit of  
A:Reference number: A48731; NCBI:93319379

T44854 poly(ADP-ribose) polymerase-1, nuclear, mitochondrial (imported) - *Archaeoglobus fulgidus* (strain ATCC 35061)  
A:Accession: T44854  
C:Date: 21-Jun-2000 sequence\_revision 21-Jun-2000 text\_change 18-Feb-2000  
R:Brandt, R.  
A:Reference number: 222860  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1202 <MON>  
A:Cross-references: EMBL:Y10817; PDB:1A04448.1

A:Genome: modA  
A:Gene: modA  
A:Note: poly(ADP-ribose) polymerase-1, nuclear, mitochondrial (imported)  
C:Keywords: poly(ADP-ribose) polymerase-1, nuclear, mitochondrial (imported)

Query Match 1.1% Score 8; DB 2; Length 260;  
Best Local Similarity 100.0%; Pred. No. 5.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 595 PRTASNF 602  
DB 53 PRTASNF 60

## RESULT 8

T30154 hypothetical protein R57.1 - *Caenorhabditis elegans*

A:Accession: T30154  
C:Date: 15-Oct-1999 sequence\_revision 15-Oct-1999 text\_change 18-Feb-2000

C:Species: *Caenorhabditis elegans*  
R:Revello, T.; Rifkin, L.; Chiappelli, B.  
A:Reference number: 220745  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-751 <FNV>  
A:Cross-references: EMBL:U88179; PDB:1A04448.1; GSPDB:GMO0208; GSPB:R57.1

A:Genome: modA  
A:Gene: R57.1  
A:Note: hypothetical protein R57.1  
A:Map position: X  
A:Instructions: 40/1; 145/1; 230/1; 313/1; 344/1; 405/1; 453/2; 576/2; 671/2; 713/3

A:Accession: A48731  
A:Residues: 1-1202 <MON>  
A:Cross-references: EMBL:U118657; NID:94981939; PDB:1A04448.1; PID:94981939

A:Note: parts of this sequence, including the amino end of the mature protein, were confirmed by peptide sequencing  
R:Gentile, S.; Bowman, S.  
A:Reference number: 549627  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1202 <MON>  
A:Cross-references: EMBL:U118657; NID:94981939; PDB:1A04448.1; PID:94981939

A:Genome: modA  
A:Gene: R57.1  
A:Note: parts of this sequence, including the amino end of the mature protein, were confirmed by peptide sequencing  
R:Gentile, S.; Bowman, S.  
A:Reference number: 549627  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1202 <MON>  
A:Cross-references: EMBL:U118657; NID:94981939; PDB:1A04448.1; PID:94981939

A:Genome: modA  
A:Gene: R57.1  
A:Note: parts of this sequence, including the amino end of the mature protein, were confirmed by peptide sequencing  
R:Gentile, S.; Bowman, S.  
A:Reference number: 549627  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1202 <MON>  
A:Cross-references: EMBL:U118657; NID:94981939; PDB:1A04448.1; PID:94981939

A:Genome: modA  
A:Gene: R57.1  
A:Note: parts of this sequence, including the amino end of the mature protein, were confirmed by peptide sequencing  
R:Gentile, S.; Bowman, S.  
A:Reference number: 549627  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1202 <MON>  
A:Cross-references: EMBL:U118657; NID:94981939; PDB:1A04448.1; PID:94981939

A:Genome: modA  
A:Gene: R57.1  
A:Note: parts of this sequence, including the amino end of the mature protein, were confirmed by peptide sequencing  
R:Gentile, S.; Bowman, S.  
A:Reference number: 549627  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1202 <MON>  
A:Cross-references: EMBL:U118657; NID:94981939; PDB:1A04448.1; PID:94981939

A:Genome: modA  
A:Gene: R57.1  
A:Note: parts of this sequence, including the amino end of the mature protein, were confirmed by peptide sequencing  
R:Gentile, S.; Bowman, S.  
A:Reference number: 549627  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1202 <MON>  
A:Cross-references: EMBL:U118657; NID:94981939; PDB:1A04448.1; PID:94981939

A:Genome: modA  
A:Gene: R57.1  
A:Note: parts of this sequence, including the amino end of the mature protein, were confirmed by peptide sequencing  
R:Gentile, S.; Bowman, S.  
A:Reference number: 549627  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1202 <MON>  
A:Cross-references: EMBL:U118657; NID:94981939; PDB:1A04448.1; PID:94981939







R Demianova, M.A.: Formosa, T.G.; Ellis, S.R.  
submitted to the EMBL Data Library, August 1995  
A:Accession: M59364  
A:Molecule type: DNA  
R:Residues: 1-252 <DBD>  
R:Cross-references: EMBL:U31756; NID:G1002791; PIDN:MAC49276.1; PID:G1002792  
R:Submitted: 1995-08-15  
R:Submitted to the EMBL Data Library, December 1995  
A:Accession: S61618  
A:Accession: S61617  
A:Molecule type: DNA  
R:Residues: 1-253 <CRB>  
A:Cross-references: EMBL:X94607; NID:G1181264; PIDN:CAA64295.1; PID:G1181269  
R:Author: B.; Urcastiau, X.A.  
A:Reference number: 564872  
A:Accession: S64876  
A:Molecule type: DNA  
R:Residues: 1-252 <NDM>  
A:Accession: S64875  
A:Reference number: 564872  
A:Accession: S64872  
A:Reference number: 564872  
A:Accession: S64872  
A:Molecule type: DNA  
A:Experimental source: strain S288C  
C:Genetics:  
A:Gene: SCD:MB1B; Y572  
A:Map position: 128  
A:Map position: 128  
A:Introns: 30/3 128  
C:Superfamily: Yeast ribosomal protein S1.e  
C:Keywords: protein biosynthesis; ribosome  
Query Match 1.0%; Score 7; DB 2; Length 252;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
oy 388 TERAEEN 394  
|||||||  
db 240 TERAEEN 246  
RESULT 31  
G72286  
C:Accession: G72286  
C:Species: Thermotoga maritima  
C:Date: 11-Jun-1999  
C:Sequence: G72286  
C:Accession: G72286  
C:Author: K.E.; Layton, R.A.; Gill, S.R.; O'Leary, M.E.; Dodson, R.J.; Hickey, P.K.; Peterson, J.D.; Wilson, M.G.  
C:Editor: M.N.; Stecher, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; Metcalberg, J.; Sutton, G.C.; Fries, C.M.  
R:Accession: J393-323-1999  
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima.

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A:Reference number: A/2200; MOTID:9928/316
A:Accession number: A/2200
A:Status: preliminary
A:Residue type: DNA
A:Residues: 1,264 <ARN>
A:Cross-reference: DB:AE00176; GB:AE000512; NID:94981619; PIDN:AD03156.1; PID:94981624; TIGR:TM1079
A:Genetic source: strain MS8
C:Genetics:
A:Gene: TM1079

Query Match
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

516 ELVERFY 522
|||||||
Db 16 ELVERFY 22

RESULT 32
T24824
hypothetical protein T11A5.5 - Caenorhabditis elegans
C:Species: C.elegans
C:Accession: C.elegans sequence revision 15-Oct-1999
C:Accession: T24824
R:McMurry, A.
submitted to the EMBL Data Library, May 1996
A:Accession: T24824
A:Accession: U59593
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residue type: DNA
A:Cross-reference: EMBL:272515; PIDN:QAA96685.1; GSPDB:GN00023; CESP:T11A5.5
A:Experimental source: clone T11A5
C:Genetics:
A:Gene: CESP:T11A5.5
A:Genetic source: strain MS8
A:Introns: 202/2

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 288;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

442 ECFGRS 448
|||||||
Db 253 ECFGRS 259

RESULT 33

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Biological process: MO281.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 sequence revision 15-Oct-1999 stxL:Change 15-Oct-1999
C:Accession: J13675
C:Length: 317
C:Submitted: 15-Oct-1999
A:Reference number: 219780
A:Accession: J13675
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Accession: J13675
A:Residues: 1313 <END>
A:Codon-references: EMBL:281107; PIDN:CA803201; CSPDB:GN0022; CSP:MO281.4
A:Experimental source: clone MO281
A:Gene: stxL
A:Accession: J13675
A:Map position: 4
A:Feature: 31/2; 195/3; 228/1

Query Match          1.0%  Score 7;  DB 2;  Length 313;
Best Local Similarity 100.0%  Pred. No. 71;
Matches 7;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

OZ  370  RTTPNS 376
DB  91  RTTPNS 97

RESULT 34
B1662
C:Probable enteromone-responsive regulatory protein X - Enterococcus faecalis
C:Species: Enterococcus faecalis
C>Date: 30-Jun-1992 stxL:Change 15-Oct-1999
C:Accession: M1662
C:Length: 1495
R:KO-S.N.: Olmsted, S.B.; Vlahova, A.S.; Gallo, J.C.; Dunny, G.M.
J. Bacteriol. 173: 7650-7664, 1991
A:Title: Molecular and genetic analysis of a region of plasmid pCF10 containing positive control genes and structural genes
A:Reference number: A1662; M1662
A:Accession: B1662
A:Status: preliminary
A:Accession: B1662
A:Residues: 1317 <END>
A:Codon-references: GB:M64978; NID:G150552; PIDN:AAA6845.1; PID:G150553
C:References:
A:Genome: A1662

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OY      600 SNFSERN    606
DB      48 SNFSERN    54

RESULT 35
B15382   cDNA-sequenced hypothetical protein - Delnoccocus radiodurans (strain RI)
C1SpecId: Delnoccocus radiodurans
C1Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #extL_change 17-Mar-2000
CAccession: B15382
R1MaltE: O.; Eissen, J.A.; Heideberg, J.P.; Hübner, E.K.; Peterson, J.D.; Dodson, R.J.; Hart, D.H.; Gysin, M.L.; Melnik, S.I.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A1Title: Genome sequence of the radioreistant bacterium Delnoccocus radiodurans RI.
AReferenceNumber: 975382
AAccession: U05382
AReleaseDate: 19990726
AStatus: preliminary
AMoleculeType: DNA
AResidueLen: 318
ASignificance: AExp001939; OB:AA000511; MID:g6459316; PID:NAPJ1121.1; PID:g6459311; TIGR:DRL560; CSPDB:GM000701
AExperimentalSource: strain RI
AGeneID: DRL560
AMapPosition: 1

Query Match
Match Local Similarity 1.0% Score 7; DB 2; Length 318;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      471 LGSNDNF    477
DB      105 LGSNDNF    111

RESULT 36
TJ5869   hypothetical protein T09B4.7 - Caenorhabditis elegans
C1SpecId: Caenorhabditis elegans
C1Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #extL_change 04-Mar-2000
CAccession: TJ5869
R1MaltE: O.; Kohnen, P.; Gillam, B.
Nucleic Acids Res 26, Suppl 2, 1169-1170, 1998
A1Title: The complete genome sequence of the nematode C. elegans.
AReferenceNumber: 320103
AAccession: TJ5869
AStatus: preliminary, translated from GR/PBMH/DBD

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AB: GN0007





Best Local Similarity 100.0%; Pred. No. 91;  
Matches 7; Conservative 0; Mismatches 0;  
Indels 0; Gaps 0;  
DB 380 ERFGLG 386  
200 ERFGLG 206

## RESULT 49

rod shape protein - Chlamydia pneumoniae (strain CW029)

C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae

C:Date: 23-Apr-1999 sequence, revision 23-Apr-1999 #text\_change 05-May-2000

C:Accession: C72026.11. M: Murthy, R.; Lamm, C.; Fan, J.; Olinger, L.; Crimwood, J.; Davis, R.W.; Stephens, R.S.

Nature Genet. 21, 385-389, 1999

A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A:Reference number: A72000; MIM:9206606

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-415 <ARN>

A:Cross-references: GB:AB001667; GB:AB001363; MIM:94377171; PID:RAD005.1; PID:94377184

A:Genetic source: strain CW029

A:Gene: RodA

C:Superfamily: rod shape-determining protein

Query Match 1.0%; Score 7; DB 2; Length 415;

Best Local Similarity 100.0%; Pred. No. 92;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 380 ERFGLG 386  
318 ERFGLG 324

RESULT 50

675363

Integral membrane protein, MRAP family - Deinococcus radiodurans (strain RJ)

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 sequence, revision 03-Dec-1999 #text\_change 17-Mar-2000

C:Accession: G75363

R:White, O.; Eilen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Hart, D.H.; Gwin, M.L.; Nelson, M.

M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Ueberlack, T.; Zalewski, C.; Makarova, K.S.; Aravind, L.; Daly, M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans RJ.

A:Reference number: A75250; MIM:2003696

A:Accession: G75363

A:Status: preliminary  
A:Molecule type: DNA  
A:Cross-references: GB:AB000012; GB:AB000513; MIM:9459473; PID:ARF1265.1; PID:9459478; TIGR:DR1709; GSPDB:GNC0077  
A:Experimental source: strain RJ  
C:Genetics: 709  
A:Gene: DR1709  
A:Superfamily: natural resistance-associated macrophage protein 1

Query Match 1.0%; Score 7; DB 2; Length 436;

Best Local Similarity 100.0%; Pred. No. 96;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 484 LCIAGCR 490  
95 LCIAGCR 101

Search completed: April 6, 2001, 16:57:03  
Job time: 151 sec





160	6	0.8	31.0	US-08-488-189-4	Sequence 12, App1
161	6	0.8	31.7	US-08-638-291-11	Sequence 12, App1
162	6	0.8	31.7	US-08-145-170-12	Sequence 12, App1
163	6	0.8	31.6	US-08-145-170-12	Sequence 12, App1
164	6	0.8	34.1	US-08-938-100-6	Sequence 2, App1
165	6	0.8	35.0	US-09-094-193-6	Sequence 6, App1
166	6	0.8	35.0	US-09-080-963-2	Sequence 2, App1
167	6	0.8	35.0	US-08-445-103-1	Sequence 1, App1
168	6	0.8	35.2	US-08-737-045-11	Sequence 11, App1
169	6	0.8	35.3	US-08-966-318-3	Sequence 3, App1
170	6	0.8	35.8	US-08-433-783-43	Sequence 43, App1
171	6	0.8	35.9	US-08-433-783-43	Sequence 43, App1
172	6	0.8	35.4	US-08-433-783-43	Sequence 43, App1
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174	6	0.8	35.7	US-08-990-319-6	Sequence 6, App1
175	6	0.8	37.0	US-08-014-338-2	Sequence 2, App1
176	6	0.8	37.0	US-08-444-189-21	Sequence 21, App1
177	6	0.8	37.0	US-08-444-189-21	Sequence 21, App1
178	6	0.8	37.3	US-09-108-020-33	Sequence 33, App1
179	6	0.8	39.1	US-07-921-118-4	Sequence 2, App1
180	6	0.8	39.1	US-08-461-603-15	Sequence 15, App1
181	6	0.8	39.1	US-08-461-603-15	Sequence 15, App1
182	6	0.8	39.2	US-08-501-003-16	Sequence 16, App1
183	6	0.8	39.7	US-08-416-000-63	Sequence 63, App1
184	6	0.8	39.7	US-08-416-000-63	Sequence 63, App1
185	6	0.8	39.7	US-08-416-000-63	Sequence 63, App1
186	6	0.8	39.3	US-08-416-000-63	Sequence 63, App1
187	6	0.8	40.5	US-08-722-719-2	Sequence 2, App1
188	6	0.8	40.5	US-08-410-982-5	Sequence 5, App1
189	6	0.8	40.5	US-08-410-982-5	Sequence 5, App1
190	6	0.8	40.5	US-08-410-982-5	Sequence 5, App1
191	6	0.8	41.4	US-08-669-408-10	Sequence 10, App1
192	6	0.8	41.4	US-08-669-408-10	Sequence 10, App1
193	6	0.8	41.3	US-08-669-408-10	Sequence 10, App1
194	6	0.8	41.7	US-08-815-463-94	Sequence 94, App1
195	6	0.8	42.1	US-09-032-312-3	Sequence 3, App1
196	6	0.8	42.3	US-08-583-118-2	Sequence 2, App1
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204	6	0.8	43.7	US-08-467-037-2	Sequence 2, App1
205	6	0.8	43.7	US-08-467-037-2	Sequence 2, App1
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208	6	0.8	43.7	US-08-919-557-91	Sequence 91, App1
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819 6 0.8 1861 2 US-07-743-206A-15 Sequence 4, Appl  
820 6 0.8 1868 1 US-08-453-702A-103 Sequence 103, Appl  
821 6 0.8 1868 1 US-08-453-702A-103 Sequence 103, Appl  
822 6 0.8 1968 2 US-08-723-305C-45 Sequence 45, Appl

APPLICATION NUMBER: US-08/528,122  
FILING DATE: 05/08/2000  
INVENTOR: EDWARD R. PITCHER  
ATTORNEY/AGENT INFORMATION: PITCHER, EDWARD R.  
REGISTRATION NUMBER: 27,829  
REFERENCE/DOCID NUMBER: PTF-001  
TRANSMISSION NUMBER: 617-248-7000  
TELEPHONE: 617-248-7000  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURES:  
NAME/KEY: Protein  
LOCATION: 1..707  
OTHER INFORMATION: PSMK  
US-08-528-122-18

Query Match Similarity 100.0%, Score 706, DB 1, Length 707.

Matches 706: Conservative 0, Mismatches 0, Indels 0, Gaps 0.

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835 6 0.8 2517 3 US-09-102-248-5 Sequence 5, Appl  
836 6 0.8 1052 2 US-08-557-122A-26 Sequence 26, Appl  
837 6 0.8 1443 2 US-08-416-603-2 Sequence 2, Appl  
838 6 0.8 4452 2 US-08-804-227C-14 Sequence 14, Appl  
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842 6 0.8 5588 2 US-08-417-113A-2 Sequence 2, Appl  
843 6 0.8 15281 2 US-08-417-113A-2 Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-08-528-122-18  
Sequence 18, Application US/08528122  
GENERAL INFORMATION:  
PATENT NO. 5176044  
APPLICANT: SUDO, KIM-HING  
TITLE OF INVENTION: EXPRESSION AND EXPORT TECHNOLOGY OF  
TITLE OF INVENTION: EXPRESSION AND EXPORT TECHNOLOGY OF  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HIRWITZ &  
ADDRESS: 125 HIGH STREET  
CITY: BOSTON  
STATE: MASS  
COUNTRY: USA  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
MEDIUM TYPE: Floppy disk  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

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DB 662 PGLYDALFTESRQDPERANGVROIVYATFOVAALETSLSEA 707

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: PITCHER, EDWARD R.  
REGISTRATION NUMBER: 27,829  
REFERENCE/DOCKET NUMBER: FIP-001  
TELEPHONE: 617-248-7000  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ. ID NO.: 18:  
SOURCE: CHAOTERISTICS:  
SEQ. ID NO.: 18  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..707  
OTHER INFORMATION: PDB:  
PDB: 0595-11720-18

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Best Local Similarity 100.0% Pct. No. 0:  
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PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/973,337A  
FILING DATE: 05 NOV 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: PITCHER, EDWARD R.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1747/41426  
TELEPHONE: 617-248-7000  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ. ID NO.: 2:  
SOURCE: CHAOTERISTICS:  
SEQ. ID NO.: 2  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-325-553-2

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Best Local Similarity 100.0% Pct. No. 0:  
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3  
US-08-325-553-2  
Sequence 2, Application US/0832553  
Patent No. 5538866  
GENERAL INFORMATION:  
NAME: PITCHER, EDWARD R.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1747/41426  
TELEPHONE: 617-248-7000  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ. ID NO.: 3:  
SOURCE: CHAOTERISTICS:  
SEQ. ID NO.: 3  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-325-553-2

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Query Match 100.0% Score 706 DB 1 Length 750:  
Best Local Similarity 100.0% Pct. No. 0:  
Matches 706: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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405 LKSGWPRFRTILASNDAREFGLASTPNAEENSRILQERGVAYINADSSIEONTLY 464



TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0523  
INVENTOR: 42253 COOP UT  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDNESS: double  
MOLECULE TYPE: linear  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
ORGANISM: Homo sapien  
TISSUE TYPE: Carcinoma  
IMMEDIATE SOURCE:  
CLONE: Prostate Specific Membrane Antigen  
US-08-325-553-11

Query Match 2.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.6e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 656 YACSPFQITDALPDIEST 674  
1 YACSPFQITDALPDIEST 19

RESULT 7  
US-08-394-152A-11  
Sequence 11; Application US/08394152A  
Patent No. 5925818  
GENERAL INFORMATION:  
APPLICANT: Israel, Ron S.  
INVENTOR: Israel, Ron S.  
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESS: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10013  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM 310 466 DX2  
OPERATING SYSTEM: PC-DOS/MS-DOS

STATE: NH  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA:  
SOFTWARE: Patent Release #1.0, Version #1.25  
APPLICATION NUMBER: US/08-622,046B  
FILING DATE: 26-MARCH-1996  
CLASSIFICATION: 514  
NAME: ROBERT A. COOPER  
REGISTRATION NUMBER: 30,440  
REFERENCE/DOCKET NUMBER: 476,001US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: 612-339-3061  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDNESS: single  
MOLECULE TYPE: linear  
US-08-622-046B-21

Query Match 2.5%; Score 18; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.6e-11;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 153 CGGATVARGVFRONT 169  
1 CGGATVARGVFRONT 18

RESULT 9  
US-08-325-553-7  
Sequence 7; Application US/08325553  
Patent No. 55946  
GENERAL INFORMATION:  
APPLICANT: Israel, Ron S.  
INVENTOR: Israel, Ron S.  
TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESS: Cooper & Dunham  
Street: 30 Rockefeller Plaza

SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
SEQUENCE 21; Application US/08622046B  
Patent No. 6103237  
CLASSIFICATION: 435  
FILING DATE: 24-FEB-95  
ATTORNEY/AGENT INFORMATION:  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41426-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 977-9550  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDNESS: double  
MOLECULE TYPE: linear  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
ORGANISM: Homo sapien  
TISSUE TYPE: Carcinoma  
IMMEDIATE SOURCE:  
CLONE: Prostate Specific Membrane Antigen  
US-08-394-152A-11

Query Match 2.7%; Score 19; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.6e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 656 YACSPFQITDALPDIEST 674  
1 YACSPFQITDALPDIEST 19

RESULT 8  
US-08-622-046B-21  
Sequence 21; Application US/08622046B  
Patent No. 6103237  
GENERAL INFORMATION:  
APPLICANT: Israel, Ron S.  
INVENTOR: Israel, Ron S.  
TITLE OF INVENTION: Stable Variant HK2 Polypeptide  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESS: Lundberg, Weesner & Kluth, P.A.  
Street: P.O. Box 2036  
CITY: Minneapolis

CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA:  
SOFTWARE: Patent Release #1.0, Version #1.25  
APPLICATION NUMBER: US/08-325,553  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41426  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 977-9550  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
STRANDNESS: double  
MOLECULE TYPE: linear  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
ORGANISM: Homo sapien  
TISSUE TYPE: Carcinoma  
IMMEDIATE SOURCE:  
CLONE: Prostate Specific Membrane Antigen  
US-08-325-553-7

Query Match 2.4%; Score 17; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 3.2e-10;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 34 TQPHLACTQFQFLAK 50  
6 TQPHLACTQFQFLAK 22

RESULT 10



US-08-394-152A-7  
 : Sequence 7, Application US/08394152A  
 : GENERAL INFORMATION:  
 : APPLICANT: Heaton, Warren D.W.  
 : APPLICANT: Heaton, Warren D.W.  
 : APPLICANT: Heaton, Warren D.W.  
 : TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND  
 : NUMBER OF SEQUENCES: 48  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESS: Cooper & Dunham LLP  
 : STREET: 1185 Avenue of the Americas  
 : CITY: New York  
 : STATE: New York  
 : COUNTRY: United States of America  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : OPERATING SYSTEM: IBM PC-DOS/MS-DOS  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/394,152A  
 : FILING DATE: 24-FEB-95  
 : CLASSIFICATION: 435  
 : ATORNEY/AGENT INFORMATION:  
 : NAME: White, John P.  
 : REFERENCE/DOCKET NUMBER: 28,678  
 : TELEPHONE: (212) 778-0400  
 : TELEFAX: (212) 391-0525  
 : INFORMATION FOR SEQ ID NO: 7:  
 : SEQUENCE CHARACTERISTICS:  
 : TYPE: amino acid  
 : STRANDEDNESS: double  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: Peptide  
 : HYPOTHEETICAL: NO  
 : AMTI-SENSE: NO  
 : ORIGINAL SOURCE:  
 : ORGANISM: Homo sapien  
 : IMMEDIATE SOURCE: Carcinoma  
 : CLONE: Prostate Specific Membrane Antigen  
 : US-08-394-152A-7

Query Match 2.4% Score 17: DB 2: Length 22:

MOLECULE TYPE: Peptide  
 : HYPOTHEETICAL: NO  
 : AMTI-SENSE: NO  
 : ORIGINAL SOURCE:  
 : ORGANISM: Homo sapien  
 : TISSUE TYPE: Carcinoma  
 : IMMEDIATE SOURCE:  
 : US-08-325-553-9  
 : Prostate Specific Membrane Antigen

Query Match 2.3% Score 16: DB 1: Length 17:  
 : Local Similarity: 100.0%, Predicted: 66.0%  
 : Matches: 16: Conservative: 0: Mismatches: 0: Indels: 0: Gaps: 0:

Qy 181 VILSDPDADYFAGVX 196  
 DB 2 VILSDPDADYFAGVX 17

US-08-394-152A-9  
 : Sequence 9, Application US/08394152A  
 : GENERAL INFORMATION:  
 : PATENT NO. 5935818  
 : APPLICANT: Heaton, Warren D.W.  
 : APPLICANT: Heaton, Warren D.W.  
 : APPLICANT: Heaton, Warren D.W.  
 : TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND  
 : NUMBER OF SEQUENCES: 48  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESS: Cooper & Dunham LLP  
 : STREET: 1185 Avenue of the Americas  
 : CITY: New York  
 : STATE: New York  
 : COUNTRY: United States of America  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : OPERATING SYSTEM: IBM PC-DOS/MS-DOS  
 : SOFTWARE: Patent In Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/394,152A  
 : FILING DATE: 24-FEB-95  
 : CLASSIFICATION: 435  
 : ATORNEY/AGENT INFORMATION:  
 : NAME: White, John P.  
 : REGISTRATION NUMBER: 28,678  
 : REFERENCE/DOCKET NUMBER: 41426-9

US-08-325-553-9  
 : Sequence 9, Application US/08325553  
 : GENERAL INFORMATION:  
 : APPLICANT: Heaton, Warren D.W.  
 : APPLICANT: Heaton, Warren D.W.  
 : APPLICANT: Heaton, Warren D.W.  
 : TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN  
 : NUMBER OF SEQUENCES: 38  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESS: Cooper & Dunham  
 : STREET: 30 Rockefeller Plaza  
 : CITY: New York  
 : STATE: New York  
 : COUNTRY: United States of America  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : OPERATING SYSTEM: IBM PC compatible  
 : SOFTWARE: Patent In Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/325,553  
 : FILING DATE:  
 : CLASSIFICATION: 435  
 : ATORNEY/AGENT INFORMATION:  
 : NAME: White, John P.  
 : REFERENCE/DOCKET NUMBER: 1747/41426  
 : TELEPHONE: (212) 977-9550  
 : TELEFAX: (212) 664-0525  
 : INFORMATION FOR SEQ ID NO: 9:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 17 amino acids  
 : TYPE: amino acid  
 : STRANDEDNESS: double  
 : TOPOLOGY: linear

TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (212) 278-0400  
 : TELEFAX: (212) 278-0400  
 : INFORMATION FOR SEQ ID NO: 9:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 17 amino acids  
 : TYPE: amino acid  
 : STRANDEDNESS: double  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: Peptide  
 : HYPOTHEETICAL: NO  
 : AMTI-SENSE: NO  
 : ORIGINAL SOURCE:  
 : ORGANISM: Homo sapien  
 : TISSUE TYPE: Carcinoma  
 : IMMEDIATE SOURCE:  
 : US-08-394-152A-9  
 : Prostate Specific Membrane Antigen

Query Match 2.3% Score 16: DB 2: Length 17:  
 : Local Similarity: 100.0%, Predicted: 66.0%  
 : Matches: 16: Conservative: 0: Mismatches: 0: Indels: 0: Gaps: 0:

Qy 181 VILSDPDADYFAGVX 196  
 DB 2 VILSDPDADYFAGVX 17

US-08-325-553-10  
 : Sequence 10, Application US/08325553  
 : GENERAL INFORMATION:  
 : PATENT NO. 5938666  
 : APPLICANT: Heaton, Warren D.W.  
 : APPLICANT: Heaton, Warren D.W.  
 : APPLICANT: Heaton, Warren D.W.  
 : TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN  
 : NUMBER OF SEQUENCES: 38  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESS: Cooper & Dunham  
 : STREET: 30 Rockefeller Plaza  
 : CITY: New York  
 : STATE: New York  
 : COUNTRY: United States of America  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : OPERATING SYSTEM: IBM PC compatible  
 : SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 FILING DATE: US/08/325,553  
 CLASSIFICATION: 435  
 PRIOR APPLICATION NUMBER: US/07/973,337A  
 ATTORNEY/AGENT INFORMATION:  
 NAME: White, John P.  
 REGISTRATION NUMBER: 28,678  
 TELEPHONE: (212) 977-9550  
 TELEFAX: (212) 664-0525  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 STRANDEDNESS: double  
 MOLECULE TYPE: peptide  
 HYPOTHEICAL: NO  
 ANTI-SENSE: NO  
 ORIGIN: human  
 ORGANISM: Homo sapien  
 TISSUE TYPE: Carcinoma  
 IMMEDIATE SOURCE:  
 CLONE: Prostate Specific Membrane Antigen

Query Match  
 Score: 2.18; Score 15; DB 1; Length 15;  
 Best Local Similarity: 100.0%; Pred. No. 2.9e-08;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 630 AFDPLDLPDPR 644  
 DB 1 AFDPLDLPDPR 15

RESULT 14  
 US-08-394-152A-10  
 Sequence 10: Application US/08394152A  
 Patent No. 5935818  
 GENERAL INFORMATION:  
 APPLICANT: Israel, Ron S.  
 APPLICANT: Heston, Warren D.W.  
 APPLICANT: Palt, William R.  
 TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND  
 TITLE OF INVENTION: USES THEREOF

US-08-325-553-8  
 Sequence 8: Application US/08325553  
 Patent No. 551866  
 GENERAL INFORMATION:  
 APPLICANT: Israel, Ron S.  
 APPLICANT: Heston, Warren D.W.  
 APPLICANT: Palt, William R.  
 TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN  
 NUMBER OF SEQUENCES: 38  
 CORRESPONDENCE ADDRESSES:  
 ADDRESS: Cooper & Dunham  
 STREET: 30 Rockefeller Plaza  
 CITY: New York  
 STATE: New York  
 COUNTRY: United States of America  
 ZIP: 10112  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/325,553  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/07/973,337A  
 ATTORNEY/AGENT INFORMATION:  
 NAME: White, John P.  
 REGISTRATION NUMBER: 28,678  
 TELEPHONE: (212) 977-9550  
 TELEFAX: (212) 664-0525  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 17 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: double  
 MOLECULE TYPE: linear  
 HYPOTHEICAL: NO  
 ANTI-SENSE: NO  
 ORIGIN: human  
 IMMEDIATE SOURCE:  
 CLONE: Prostate Specific Membrane Antigen

NUMBER OF SEQUENCES: 48  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Cooper & Dunham LLP  
 STREET: 110 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: United States of America  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/394,152A  
 FILING DATE: 24-FEB-95  
 ATTORNEY/AGENT INFORMATION:  
 NAME: White, John P.  
 REGISTRATION NUMBER: 28,678  
 TELEPHONE: (212) 977-9550  
 TELEFAX: (212) 391-0525  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHEICAL: NO  
 ANTI-SENSE: NO  
 ORIGIN: human  
 IMMEDIATE SOURCE:  
 CLONE: Prostate Specific Membrane Antigen

Query Match  
 Score: 2.18; Score 15; DB 2; Length 15;  
 Best Local Similarity: 100.0%; Pred. No. 2.9e-08;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 630 AFDPLDLPDPR 644  
 DB 1 AFDPLDLPDPR 15

US-08-394-152A-8  
 Sequence 8: Application US/08394152A  
 Patent No. 5935818  
 GENERAL INFORMATION:  
 APPLICANT: Israel, Ron S.  
 APPLICANT: Heston, Warren D.W.  
 APPLICANT: Palt, William R.  
 TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND  
 TITLE OF INVENTION: USES THEREOF  
 NUMBER OF SEQUENCES: 48  
 CORRESPONDENCE ADDRESSES:  
 ADDRESS: Cooper & Dunham LLP  
 STREET: 110 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: United States of America  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/394,152A  
 FILING DATE: 24-FEB-95  
 ATTORNEY/AGENT INFORMATION:  
 NAME: White, John P.  
 REGISTRATION NUMBER: 28,678  
 TELEPHONE: (212) 977-9550  
 TELEFAX: (212) 391-0525  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 17 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear

MOLECULE TYPE: Peptide  
 AMINO ACIDS: 12  
 AMTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapien  
 TISSUE TYPE: Carcinoma  
 IMMEDIATE SOURCE:  
 CLONE: Prostate Specific Membrane Antigen  
 US-08-394-152A-8

Query Match 2.0% Score 14: DB 2: Length 17:  
 Best Local Similarity 100.0% Pred. No. 2.9e-07:  
 Matches 14: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 180 RTTLPASDAE 193  
 DB 1 RTTLPASDAE 14

RESULT 17  
 US-08-325-553-34  
 Sequence 34, Application US/08325553  
 Patent No. 5538866  
 GENERAL INFORMATION:  
 APPLICANT: Heaton, Warren D. W.  
 APPLICANT: Falt, William R.  
 TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN  
 NUMBER OF SEQUENCES: 38  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Cooper & Dunham  
 STREET: 30 Rockefeller Plaza  
 CITY: New York  
 STATE: New York  
 COUNTRY: United States of America  
 ZIP: 10112  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/325,553  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/07/973,337A  
 FILING DATE: 05 NOV 1992  
 ATORNEY/AGENT INFORMATION:  
 NAME: White, John P.

MEDIUM TYPE: floppy disk  
 COMPUTER: IBM 330 466 DX2  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/394,152A  
 FILING DATE: 24-FEB-95  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 NAME: White, John P.  
 REGISTRATION NUMBER: 28,678  
 REFERENCE/DOCKET NUMBER: 41426-B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 391-0520  
 TELEFAX: (212) 391-0523  
 INFORMATION FOR SEQ ID NO: 34:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 12 amino acids  
 TYPE: amino acid acids  
 STRANDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 AMINO ACIDS: 12  
 AMTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo Sapien  
 TISSUE TYPE: Carcinoma  
 IMMEDIATE SOURCE:  
 CLONE: Prostate Specific Membrane Antigen  
 US-08-394-152A-34

Query Match 1.7% Score 12: DB 2: Length 12:  
 Best Local Similarity 100.0% Pred. No. 2.9e-05:  
 Matches 12: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 370 RTTLPASDAE 381  
 DB 1 RTTLPASDAE 12

RESULT 19  
 US-08-325-553-31  
 Sequence 31, Application US/08325553  
 Patent No. 5538866  
 GENERAL INFORMATION:  
 APPLICANT: Heaton, Warren D. W.  
 APPLICANT: Falt, William R.  
 TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN  
 NUMBER OF SEQUENCES: 38

REGISTRATION NUMBER: 28,678  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 977-9550  
 TELEFAX: (212) 664-0525  
 INVENTION INFORMATION:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 12 amino acids  
 TYPE: amino acid  
 STRANDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 AMTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo Sapien  
 CELL TYPE: Carcinoma  
 IMMEDIATE SOURCE:  
 CLONE: Prostate Specific Membrane Antigen  
 US-08-325-553-34

Query Match 1.7% Score 12: DB 1: Length 12:  
 Best Local Similarity 100.0% Pred. No. 2.9e-05:  
 Matches 12: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 370 RTTLPASDAE 381  
 DB 1 RTTLPASDAE 12

RESULT 18  
 US-08-394-152A-34  
 Sequence 34, Application US/08394152A  
 Patent No. 5538866  
 GENERAL INFORMATION:  
 APPLICANT: Heaton, Warren D. W.  
 APPLICANT: Falt, William R.  
 TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND  
 NUMBER OF SEQUENCES: 48  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Cooper & Dunham LLP  
 STREET: 1185 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: United States of America  
 ZIP: 10105  
 COMPUTER READABLE FORM:

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Cooper & Dunham  
 STREET: 30 Rockefeller Plaza  
 CITY: New York  
 STATE: New York  
 COUNTRY: United States of America  
 ZIP: 10112  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 OPERATING SYSTEM: IBM PC Compatible  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/325,553  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA: US/07/973,337A  
 FILING DATE: 05 NOV 1992  
 ATORNEY/AGENT INFORMATION:  
 NAME: White, John P.  
 REGISTRATION NUMBER: 28,678  
 REFERENCE/DOCKET NUMBER: 41426  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 977-9550  
 TELEFAX: (212) 664-0525  
 INFORMATION FOR SEQ ID NO: 31:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 STRANDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 AMTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo Sapien  
 TISSUE TYPE: Carcinoma  
 IMMEDIATE SOURCE:  
 CLONE: Prostate Specific Membrane Antigen  
 US-08-325-553-31

Query Match 1.3% Score 9: DB 1: Length 9:  
 Best Local Similarity 100.0% Pred. No. 1.3e-05:  
 Matches 9: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 42 TEOQPOLAK 50  
 DB 1 TEOQPOLAK 9

RESULT 20  
 US-08-325-553-31  
 Sequence 31, Application US/08325553  
 Patent No. 5538866  
 GENERAL INFORMATION:  
 APPLICANT: Heaton, Warren D. W.  
 APPLICANT: Falt, William R.  
 TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN  
 NUMBER OF SEQUENCES: 38

RESULT 20  
US-08-394-152A-31  
Sequence 31: Application US/08394152A  
Patent No. 6150508  
GENERAL INFORMATION:  
APPLICANT: Isarelli, Ron S.  
APPLICANT: Falt, William R.  
APPLICANT: Hascon, Warren D.W.  
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM 310 466 DX2  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASTED for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/394,152A  
FILING DATE: 24 FEB 95  
PRIORITY DATE: 13 FEB 95  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/OCCKET NUMBER: 4126-B  
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN  
TELEPHONE: (212) 391-0523  
TELEFAX: (212) 391-0523  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 481  
TYPE: amino acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
METHOD OF PREP: Peptide  
HYPOTHETICAL: NO  
ORIGINAL SOURCE: NO  
ORGANISM: Homo Sapien  
IMMEDIATE SOURCE: Carcinoma  
CLONE: Prostate Membrane Specific Antigen  
US-08-394-152A-31

Query Match 1.38: Score 9, DB 3, Length 481:  
Best Local Similarity 100.0%, Pred. No. 0.87, 0, Indels 0, Gaps 0,  
Matches 5, Conservative 0, Mismatches 0  
CY 379 AERFGLGS 387  
DB 276 AERFGLGS 284

RESULT 23  
US-09-044-668-1  
Sequence 1: Application US/09044668  
Patent No. 6150508  
GENERAL INFORMATION:  
APPLICANT: Murphy, Gerald P.  
APPLICANT: Boynton, Alton L.  
APPLICANT: Hascon, Warren D.W.  
APPLICANT: Falt, William R.  
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC  
FOR THE EXTRACELLULAR DOMAIN OF PROSTATE-SPECIFIC  
MEMBRANE ANTIGEN  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Peptide & Edmonds, LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FASTED for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/044,668  
FILING DATE: 18 MAR 1998  
CLASSIFICATION: 536

Query Match 1.38: Score 9, DB 2, Length 9:  
Best Local Similarity 100.0%, Pred. No. 1.3e+05,  
Matches 9, Conservative 0, Mismatches 0, Indels 0,  
Gaps 0  
CY 42 TEORQLAK 50  
DB 1 TEORQLAK 9

RESULT 21  
US-09-330-095-6  
Sequence 6: Application US/09330095  
Patent No. 6127161  
GENERAL INFORMATION:  
APPLICANT: Kikkawa Corporation  
TITLE OF INVENTION: Lencine Antipeptidase Gene, Recombinant DNA, and  
Process for Producing Lencine Antipeptidase  
FILE REFERENCE: PR-622  
REGISTRATION NUMBER: US/09/330,095  
CURRENT FILING DATE: 1998-06-12  
EARLIER FILING DATE: 1998-06-12  
NUMBER OF SEQ ID NOS: 14  
SEQ ID NO 6  
TITLE OF INVENTION: Lencine Antipeptidase Gene, Recombinant DNA, and  
Process for Producing Lencine Antipeptidase  
FILE REFERENCE: PR-622  
US-09-330-095-6

Query Match 1.38: Score 8, DB 3, Length 8:  
Best Local Similarity 100.0%, Pred. No. 1.3e+05,  
Matches 8, Conservative 0, Mismatches 0, Indels 0,  
Gaps 0  
CY 672 ESTVDPK 679  
DB 1 ESTVDPK 8

RESULT 24  
US-08-325-553-6  
Sequence 6: Application US/08325533  
Patent No. 553866  
GENERAL INFORMATION:  
APPLICANT: Isarelli, Ron S.  
APPLICANT: Hascon, Warren D.W.  
APPLICANT: Falt, William R.  
TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
INVENTOR: 581815  
FILING DATE: US/08/325,553  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: US/07/973,337A  
APPLICATION NUMBER: US/07/973,337A  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1747/41426  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
IMMEDIATE SOURCE: 6  
IMMEDIATE SOURCE: 6  
SOURCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STANDARDNESS: double  
MOLECULE TYPE: linear  
HYPOTHEICAL: NO  
AMTI-SENSE: NO  
ORIGINAL SOURCE: 6  
TISSUE TYPE: Carcinoma  
IMMEDIATE SOURCE:  
CLONE: Prostate Specific Membrane Antigen  
US-08-325-553-6

Query Match 1.1% Score 8; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1,3e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 311 IYNYIGTL 318  
DB 1 IYNYIGTL 8

RESULT 25  
US-08-394-152A-6  
Sequence 6, Application US/08394152A  
INVENTOR: 581815  
GENERAL INFORMATION:  
APPLICANT: Heaton, Warren D.W.  
ADDRESS: 30 Cockfeller Plaza  
CITY: New York  
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND

RESULT 26  
US-08-793-824-2  
Sequence 2, Application US/08793824  
INVENTOR: 581815  
GENERAL INFORMATION:  
APPLICANT: Simpson, Christine Lynn  
ADDRESS: 1000 15th Avenue  
CITY: New York  
TITLE OF INVENTION: Increase stored Catbonydates  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESS: 1000 15th Avenue  
CITY: New York  
STREET: Level 8, 1168 Walker Street  
CITY: No. 5981815th Sydney  
STATE: New South Wales  
COUNTRY: Australia  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
SOFTWARE: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793,824  
FILING DATE: 05/08/325,553  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU P7643  
FILING DATE: 24-NOV-1994  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: 61 2 957 6288  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STANDARDNESS:  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus salivarius  
US-08-793-824-2

Query Match 1.1% Score 8; DB 2; Length 1577;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 16 AFIDELEA 23

TITLE OF INVENTION: USES THEREOF  
NUMBER OF SEQUENCES: 48  
INVENTOR: 581815  
COMPILED BY: Cooper & Dunham LLP  
ADDRESS: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
SOFTWARE: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/394,152A  
FILING DATE: 05/08/325,553  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1747/41426  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STANDARDNESS: double  
MOLECULE TYPE: linear  
HYPOTHEICAL: NO  
AMTI-SENSE: NO  
ORIGINAL SOURCE: 6  
TISSUE TYPE: Carcinoma  
IMMEDIATE SOURCE:  
CLONE: Prostate Specific Membrane Antigen  
US-08-394-152A-6

Query Match 1.1% Score 8; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1,3e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 311 IYNYIGTL 318  
DB 1 IYNYIGTL 8

DB 1091 AFIDELEA 1098  
RESULT 27  
US-08-325-553-5  
Sequence 5, Application US/08325553  
INVENTOR: 581815  
GENERAL INFORMATION:  
APPLICANT: Heaton, Warren D.W.  
ADDRESS: 30 Cockfeller Plaza  
CITY: New York  
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESS: 30 Cockfeller Plaza  
CITY: New York  
STREET: 30 Cockfeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/325,553  
FILING DATE: 05/08/325,553  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: US/07/973,337A  
FILING DATE: 05 NOV 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1747/41426  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STANDARDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
ORIGINAL SOURCE:

ORGANISM: Homo sapien  
TISSUE TYPE: Carcinoma  
IMMEDIATE SOURCE:  
CLONE: Prostate Specific Membrane Antigen  
US-08-355-5

Query Match 1.0% Score 7; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred No. 1.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 521 PROPMK 527  
DB 1 PROPMK 7

RESULT 28  
US-08-394-152A-5  
US-08-394-152A-5 Application US/08/94152A  
Patent No. 5935618  
GENERAL INFORMATION:  
APPLICANT: Israel, Ron S.  
APPLICANT: Heston, Warren D. W.  
APPLICANT: Heston, Warren D. W.  
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND  
TITLE OF INVENTION: USES THEREOF  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS: Dunham LLP  
ADDRESS: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: IBM compatible  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/394,152A  
APPLICATION NUMBER: US/08/394,152A  
CLASSIFICATION: 435-95  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE NUMBER: 11136-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 351-0525  
INFORMATION FOR SEQ ID NO: 5:

FILING DATE: 07-OCT-1996  
APPLICATION NUMBER: 08/729,743  
FILING DATE: 10-JUL-1996  
APPLICATION NUMBER: 08/567,357  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: 08/448,498  
FILING DATE: 02-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Hall, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE NUMBER: 07/657,40001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
MOLECULAR TYPE: Peptide  
US-08-946-329A-82

Query Match 1.0% Score 7; DB 3; Length 106;  
Best Local Similarity 100.0%; Pred No. 2.2e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 22 KABINK 28  
DB 44 KABINK 50

RESULT 30  
US-08-970-131-3  
US-08-970-131-3 Application US/08/970133  
Patent No. 5916753  
GENERAL INFORMATION:  
APPLICANT: Geigley, Karl J.  
APPLICANT: Geigley, Karl J.  
TITLE OF INVENTION: SH3-CONTAINING PROTEINS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESS: Incyte Pharmaceuticals, Inc.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette

SEQUENCE CHARACTERISTICS:  
LENGTH: 175 amino acids  
TYPE: amino acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULAR TYPE: peptide  
HYDROPHATIC: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapien  
TISSUE TYPE: Carcinoma  
IMMEDIATE SOURCE:  
CLONE: Prostate Specific Membrane Antigen  
US-08-394-152A-5

Query Match 1.0% Score 7; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred No. 1.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 521 PROPMK 527  
DB 1 PROPMK 7

RESULT 29  
US-08-946-329A-82  
US-08-946-329A-82 Application US/08/946329A  
Patent No. 6023952  
GENERAL INFORMATION:  
APPLICANT: Beachy, Philip A.  
APPLICANT: Porter, Jeffrey A.  
TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:  
ADDRESS: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: diskette  
OPERATING SYSTEM: IBM compatible  
SOFTWARE: FASTSD for Windows Version 2.0b  
CURRENT APPLICATION DATA: US/08/946,329A  
APPLICATION NUMBER: US/08/946,329A  
FILING DATE: 09-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/061,323

COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS Windows Version 2.0  
SOFTWARE: FASTSD for Windows Version 2.0b  
CURRENT APPLICATION DATA: US/08/970,133  
FILING DATE: Filed Heston  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hall, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: PF-0419 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 175 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: PROSNT70  
US-08-970-131-3

Query Match 1.0% Score 7; DB 2; Length 175;  
Best Local Similarity 100.0%; Pred No. 1.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 268 SAPPDS 274  
DB 69 SAPPDS 75

RESULT 31  
US-08-353-197A-2  
US-08-353-197A-2 Application US/08/353197A  
Patent No. 6023952  
GENERAL INFORMATION:  
APPLICANT: Melner, Joel E.  
APPLICANT: Melner, Joel E.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PROTEIN  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS: Carroll, LLP  
ADDRESS: 220 Montgomery Street, Suite 2200  
CITY: San Francisco

STATE: California  
COUNTRY: United States of America  
ZIP: 94104  
COMPUTER: IBM PC compatible  
MEDIUM TYPE: 3.5 INCH DISKETTE  
OPERATING SYSTEM: MS-DOS  
CURRENT APPLICATION DATA: US 60/020,003  
APPLICATION NUMBER: US 60/020,003  
CLASSIFICATION: 435  
FILING DATE: 01-APR-1996  
PRIORITY DATE: 01-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: MARGARET T. KAMRIN  
REFERENCE/DOCKET NUMBER: DALB-01393  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 397-8338  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
TYPE: amino acid  
STRANDNESS: not relevant  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-468-847B-13

Query Match 1.0%; Score 7; DB 3; Length 284;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 231 MATCHES 237

RESULT 32  
US-08-468-847B-13  
Sequence 16, Application US/08468847B  
Patent No. 5786263  
GENERAL INFORMATION:  
APPLICANT: Hastings, Gregg A. and Adams, Mary D.  
TITLE OF INVENTION: Human CCR-like G-protein factor  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARRELLA, BYRNE, BAIN, GILFILLAN,  
APPLICANT: CECCHI, STEWART & OLSTEIN  
ADDRESS: 520 White Plains Road, P.O. Box 2005  
CITY: Tarrytown  
STATE: NY  
COUNTRY: USA  
ZIP: 10591-9005  
COMPUTER: IBM PC compatible  
MEDIUM TYPE: 3.5 INCH DISKETTE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA: US 60/013,612  
APPLICATION NUMBER: US 60/013,612  
CLASSIFICATION: 435  
FILING DATE: 28-FEB-1996  
PRIORITY DATE: 28-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REFERENCE/DOCKET NUMBER: CGC 1847  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8689  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
TYPE: amino acid  
STRANDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
US-08-808-931-16

TITLE OF INVENTION: DNA Molecules Encoding Plant  
TITLE OF INVENTION: Protoporphyrinogen Oxidase and Inhibitor-Resistant Mutants  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 593602artis Corporation  
STREET: 520 White Plains Road, P.O. Box 2005  
CITY: Tarrytown  
STATE: NY  
COUNTRY: USA  
ZIP: 10591-9005  
COMPUTER: IBM PC compatible  
MEDIUM TYPE: 3.5 INCH DISKETTE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA: US 60/013,612  
APPLICATION NUMBER: US 60/013,612  
CLASSIFICATION: 435  
FILING DATE: 28-FEB-1996  
PRIORITY DATE: 28-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REFERENCE/DOCKET NUMBER: CGC 1847  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8689  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
TYPE: amino acid  
STRANDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
US-08-808-931-16

Query Match 1.0%; Score 7; DB 2; Length 339;  
Best Local Similarity 100.0%; Pred. No. 1;e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 102 PREPOTYPE 108

STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07066  
COMPUTER: IBM PC compatible  
MEDIUM TYPE: 3.5 INCH DISKETTE  
OPERATING SYSTEM: MS-DOS  
CURRENT APPLICATION DATA: US 60/020,003  
APPLICATION NUMBER: US 60/020,003  
CLASSIFICATION: 435  
FILING DATE: 01-APR-1996  
PRIORITY DATE: 01-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: MARGARET T. KAMRIN  
REFERENCE/DOCKET NUMBER: DALB-01393  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 397-8338  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
TYPE: amino acid  
STRANDNESS: not relevant  
TOPOLOGY: unknown  
MOLECULE TYPE: PROTEIN  
US-08-468-847B-13

Query Match 1.0%; Score 7; DB 1; Length 375;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 284 TRKSPSP 290

RESULT 33  
US-08-808-931-16  
Sequence 16, Application US/08808931  
Patent No. 5786263  
GENERAL INFORMATION:  
APPLICANT: Hastings, Gregg A. and Adams, Mary D.  
TITLE OF INVENTION: Human CCR-like G-protein factor  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARRELLA, BYRNE, BAIN, GILFILLAN,  
APPLICANT: CECCHI, STEWART & OLSTEIN  
ADDRESS: 520 White Plains Road, P.O. Box 2005  
CITY: Tarrytown  
STATE: NY  
COUNTRY: USA  
ZIP: 10591-9005  
COMPUTER: IBM PC compatible  
MEDIUM TYPE: 3.5 INCH DISKETTE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA: US 60/013,612  
APPLICATION NUMBER: US 60/013,612  
CLASSIFICATION: 435  
FILING DATE: 28-FEB-1996  
PRIORITY DATE: 28-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REFERENCE/DOCKET NUMBER: CGC 1846  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8689  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
TYPE: amino acid

TITLE OF INVENTION: DNA Molecules Encoding Plant  
TITLE OF INVENTION: Protoporphyrinogen Oxidase and Inhibitor-Resistant Mutants  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 593602artis Corporation  
STREET: 520 White Plains Road, P.O. Box 2005  
CITY: Tarrytown  
STATE: NY  
COUNTRY: USA  
ZIP: 10591-9005  
COMPUTER: IBM PC compatible  
MEDIUM TYPE: 3.5 INCH DISKETTE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA: US 60/013,612  
APPLICATION NUMBER: US 60/013,612  
CLASSIFICATION: 435  
FILING DATE: 28-FEB-1996  
PRIORITY DATE: 28-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REFERENCE/DOCKET NUMBER: CGC 1846  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8689  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
TYPE: amino acid

STRANDNESS: not relevant  
TOPOLGY: not relevant  
MOLECULE TYPE: protein  
US-08-403-803-2

Query Match 1.0%; Score 7; DB 3; Length 539;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 187 PEPHYE 193

RESULT 35  
US-09-050-603A-16  
US-09-050-603A-16 Application US/09050603A  
Patent No. 6021012  
GENERAL INFORMATION:  
APPLICANT: Volinath, Sandra  
APPLICANT: Johnson, Marie  
APPLICANT: Johnson, Marie  
APPLICANT: Ward, Eric  
APPLICANT: Helfetz, Peter  
TITLE OF INVENTION: DNA Molecules Encoding Plant  
PROTEIN ENDOGENOUS PHOTOPHYTYLASE  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSER: No. 6021012Article Corporation  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/050/603A  
FILING DATE: 30-MAR-1998  
CLASSIFICATION: B00  
PRIOR APPLICATION DATA: US 09/008,931  
FILING DATE: 28-FEB-1997  
PRIOR APPLICATION DATA: US 60/012,705  
FILING DATE: 28-FEB-1996  
PRIOR APPLICATION DATA:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/102/4208  
FILING DATE: 22-JUN-1998  
CLASSIFICATION: B00  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/059,164  
FILING DATE: 13-APR-1998  
PRIOR APPLICATION DATA: US 09/050,603  
FILING DATE: 30-MAR-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/126,430  
FILING DATE: 11-MAR-1998  
PRIOR APPLICATION DATA: US 09/808,931  
FILING DATE: 28-FEB-1997  
PRIOR APPLICATION DATA: US 60/012,705  
FILING DATE: 28-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/013,612  
FILING DATE: 11-FEB-1996  
PRIOR APPLICATION DATA: US 60/020,003  
FILING DATE: 21-JUN-1996  
PRIOR APPLICATION DATA: US 08/472,028  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Heiga, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: 19226/580 (R-5228)  
TELEPHONE: (919) 541-8587  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
TYPE: amino acids  
LENGTH: 539 amino acids  
STRANDNESS: not relevant  
MOLECULE TYPE: protein  
US-09-102-4208-16

Query Match 1.0%; Score 7; DB 3; Length 539;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

APPLICATION NUMBER: US 60/013,612  
PRIOR APPLICATION DATA: US 60/020,003  
FILING DATE: 21-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Heiga, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: 19226/580 (R-5228)  
TELEPHONE: (919) 541-8587  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
TYPE: amino acids  
LENGTH: 539 amino acids  
STRANDNESS: not relevant  
MOLECULE TYPE: protein  
US-09-050-603A-16

Query Match 1.0%; Score 7; DB 3; Length 539;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 187 PEPHYE 193

RESULT 36  
US-09-102-4208-16  
US-09-102-4208-16 Application US/091024208  
Patent No. 6084155  
GENERAL INFORMATION:  
APPLICANT: Volinath, Sandra  
APPLICANT: Johnson, Marie  
APPLICANT: Johnson, Marie  
APPLICANT: Ward, Eric  
APPLICANT: Helfetz, Peter  
TITLE OF INVENTION: HERBICIDE-TOLERANT PHOTOPHYTYLASE  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSER: No. 6084155Article Corporation  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER: READABLE FORM:

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 187 PEPHYE 193

RESULT 37  
US-08-547-197-1  
US-08-547-197-1 Application US/08547197  
Patent No. 608115  
GENERAL INFORMATION:  
APPLICANT: Gong, Joseph K.  
APPLICANT: Gong, Joseph K.  
APPLICANT: Gong, Joseph K.  
TITLE OF INVENTION: EXPOSURE TO RADIATION OR RADIONUCLIDIC AGENTS  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Nikon, Haisave, Devana & Doyle LLP  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/547,197  
FILING DATE: 08/05/97  
ATTORNEY/AGENT INFORMATION:  
NAME: Rogalsky, Peter  
REGISTRATION NUMBER: 38,601  
REFERENCE/DOCKET NUMBER: 19226/580 (R-5228)  
TELEPHONE: (716) 263-1640  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
TYPE: amino acids  
LENGTH: 102  
STRANDNESS: single  
MOLECULE TYPE: linear  
US-08-547-197-1

Query Match 1.0%; Score 7; DB 1; Length 622;





COUNTRY: United States of America  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 CURRENT APPLICATION DATA: Release #1.0, Version #1.25  
 APPLICATION NUMBER: US/08/325,553  
 FILING DATE: 24 FEB 95  
 PRIORITY INFORMATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/07/973,337A  
 FILING DATE: 05 NOV 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Heaton, Warren D. M.  
 REGISTRATION NUMBER: 28,678  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 664-0525  
 TELEFAX: (212) 664-0525  
 TELETYPE: 422523 COOP UT  
 INFORMATION FOR SEQ ID NO: 37:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHEICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 CELL TYPE: Homo sapien  
 IMMEDIATE SOURCE:  
 CLONE: Prostate Specific Membrane Antigen  
 US-08-325-553-37

Query Match 0.84; Score 6; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred No. 1,3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 438 RSPD80 443  
 OY 111111  
 DB 1 RSPD80 6  
 RESULT 42  
 US-08-394-152A-35  
 Sequence 35, Application US/08394152A

Mon Apr 9 11:14:12 2001 us-08-403-803-2\_copy\_45\_750.olly.rsl

OY 19 DEKAE 24  
 DB 1 DEKAE 6  
 RESULT 43  
 US-08-394-152A-36  
 Sequence 36, Application US/08394152A  
 GENERAL INFORMATION:  
 APPLICANT: Heaton, Warren D. M.  
 APPLICANT: Heaton, Warren D. M.  
 TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND  
 NUMBER OF SEQUENCES: 48  
 CORRESPONDENCE ADDRESS:  
 STREET: 1185 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: United States of America  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/394,152A  
 FILING DATE: 24 FEB 95  
 PRIORITY INFORMATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Heaton, Warren D. M.  
 REGISTRATION NUMBER: 28,678  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 278-0400  
 TELEFAX: (212) 391-0525  
 INFORMATION FOR SEQ ID NO: 36:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHEICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapien

PATENT No. 5935818  
 GENERAL INFORMATION:  
 APPLICANT: Heaton, Warren D. M.  
 APPLICANT: Heaton, Warren D. M.  
 TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND  
 NUMBER OF SEQUENCES: 48  
 CORRESPONDENCE ADDRESS:  
 STREET: 1185 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: United States of America  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/394,152A  
 FILING DATE: 24 FEB 95  
 PRIORITY INFORMATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Heaton, Warren D. M.  
 REGISTRATION NUMBER: 28,678  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 278-0400  
 TELEFAX: (212) 391-0525  
 INFORMATION FOR SEQ ID NO: 35:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHEICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 CELL TYPE: Homo sapien  
 IMMEDIATE SOURCE:  
 CLONE: Prostate Specific Membrane Antigen  
 US-08-394-152A-35

Mon Apr 9 11:14:12 2001 us-08-403-803-2\_copy\_45\_750.olly.rsl

CELL TYPE: Carcinoma  
 IMMEDIATE SOURCE:  
 CLONE: Prostate Specific Membrane Antigen  
 US-08-394-152A-36  
 Query Match 0.84; Score 6; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred No. 1,3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 88 MEDCNE 93  
 DB 1 MEDCNE 6  
 RESULT 44  
 US-08-394-152A-37  
 Sequence 37, Application US/08394152A  
 GENERAL INFORMATION:  
 APPLICANT: Heaton, Warren D. M.  
 APPLICANT: Heaton, Warren D. M.  
 TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND  
 NUMBER OF SEQUENCES: 48  
 CORRESPONDENCE ADDRESS:  
 STREET: 1185 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: United States of America  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/394,152A  
 FILING DATE: 24 FEB 95  
 PRIORITY INFORMATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Heaton, Warren D. M.  
 REGISTRATION NUMBER: 28,678  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 278-0400  
 TELEFAX: (212) 391-0525  
 INFORMATION FOR SEQ ID NO: 37:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHEICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 CELL TYPE: Homo sapien  
 IMMEDIATE SOURCE:  
 CLONE: Prostate Specific Membrane Antigen  
 US-08-394-152A-37

LENGTH: 6 amino acids  
TYPE: amino acid  
STANDARDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYDROPHOBICITY: NO  
ANTISENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapien  
CELL TYPE: Carcinoma  
INSTRUMENT: 433  
CLONE: Prostate Specific Membrane Antigen  
US-08-394-152A-37

Query Match  
Best Local Similarity 100.0%  
Matches 6: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 438 RESIDUE 443  
DB 1 RESIDUE 6

RESULT 45  
US-07-968-781A-12  
Sequence 12, Application US/07968781A  
Patent No. 5430137

GENERAL INFORMATION:  
APPLICANT: Sietze, Frank H.  
ATTORNEY/AGENT INFORMATION:  
APPLICANT: Thompson, Mark  
APPLICANT: Schepf, H. Ernest  
APPLICANT: Schepf, George E.  
TITLE OF INVENTION: Method for the identification of Bacillus  
TITLE OF INVENTION: Huntington's Endotoxin Genes  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
STREET: 2412 N.W. 1st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: USA  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
SOFTWARE: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA: Release #1.0, Version #1.25

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: PC/CT/US92/10068  
FILING DATE: 19921120  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
CLASSIFICATION: US 07/798, 221  
FILING DATE: 22-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: SCR221P  
TELEPHONE: 619-554-2837  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 4:  
LENGTH: 10 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYDROPHOBICITY: NO  
ANTISENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Region  
CELL TYPE: Region  
INSTRUMENT: 1  
CLONE: "Added amino-terminal"  
OTHER INFORMATION: "glycine residue"  
OTHER INFORMATION: "note" "Added carboxy-terminal"  
OTHER INFORMATION: "glycine residue"  
PCT-US93-10068-4

Query Match  
Best Local Similarity 100.0%  
Matches 6: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 442 RESIDUE 447  
DB 3 RESIDUE 8

RESULT 47  
US-08-305-871A-28  
Sequence 12, Application US/08305871A  
Patent No. 5736142

APPLICATION NUMBER: US/07/968,781A  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Salviach, David R.  
REGISTRATION NUMBER: 21,744,444, PPOCI  
TELEPHONE: 904-375-8100  
TELEFAX: 904-375-8800  
INSTRUMENT: 433  
CLONE: Prostate Specific Membrane Antigen  
US-07-968-781A-12

Query Match  
Best Local Similarity 100.0%  
Matches 6: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 286 RESIDUE 291  
DB 1 RESIDUE 6

RESULT 46  
US-07-968-781A-12  
Sequence 4, Application PC/TUS9210068  
Patent No. 5430137  
GENERAL INFORMATION:  
APPLICANT: Aletti, Dario C  
ATTORNEY/AGENT INFORMATION:  
APPLICANT: Schepf, George E.  
APPLICANT: Schepf, H. Ernest  
TITLE OF INVENTION: Factor X-Derived Polypeptides and  
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
STREET: Office of Patent Counsel, The Scripps  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
SOFTWARE: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA: Release #1.0, Version #1.30  
FILING DATE: 14-SEP-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
CLASSIFICATION: US 08/121,101  
FILING DATE: 14-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,714,137-0062-10  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0100  
INSTRUMENT: 433  
CLONE: "Tyrosine or phenylalanine"  
OTHER INFORMATION: "tyrosine or phenylalanine"  
PCT-US-93-10068-4

GENERAL INFORMATION:  
APPLICANT: Sietze, Alessandro  
ATTORNEY/AGENT INFORMATION:  
APPLICANT: Schepf, George E.  
APPLICANT: Schepf, H. Ernest  
TITLE OF INVENTION: Alteration of Immune Response Using Pan  
TITLE OF INVENTION: Binding Peptides  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
STREET: Townsend and Townsend and Crew LLP  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US 08/305,871A  
FILING DATE: 14-SEP-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
CLASSIFICATION: US 08/121,101  
FILING DATE: 14-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,714,137-0062-10  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0100  
INSTRUMENT: 433  
CLONE: "Tyrosine or phenylalanine"  
OTHER INFORMATION: "tyrosine or phenylalanine"  
PCT-US-93-10068-4

Query Match  
Best Local Similarity 100.0%  
Matches 6: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 286 RESIDUE 291  
DB 1 RESIDUE 6

RESULT 48  
US-08-305-871A-28  
Sequence 12, Application US/08305871A  
Patent No. 5736142

Best Local Similarity 100.0% Pred No. 32:  
Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
QY 697 AAETL 702  
DB 4 AAETL 9

RESULT 48  
US-08-164-618-1  
Sequence 1: Application US/08164618  
Patent No. 5408036  
GENERAL INFORMATION:  
APPLICANT: Gabel, M. Reza  
TITLE OF INVENTION: Compositions and Synthetic Methods  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Dresser, Coldmalt, Shore, Suter &  
STREET: 180 No. 5408036th Street, Suite 4700  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
SOFTWARE: IBM PC compatible  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/164.618  
FILING DATE: 05/07/1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 510  
FILING DATE: 05/07/1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/591,988  
FILING DATE: 05/07/1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Gerson, Edward G.  
REGISTRATION NUMBER: 29,381  
TELEPHONE: (312) 616-5400  
TELEFAX: (312) 616-5460  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-156-552A-9  
Query Match 0.8% Score 6: DB 1: Length 16:  
Best Local Similarity 100.0% Pred No. 39:  
Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
QY 258 AAKLE 263  
DB 3 AAKLE 8

RESULT 50  
US-08-477-509B-112  
Sequence 1: Application US/08477509B  
Patent No. 5770697  
GENERAL INFORMATION:  
APPLICANT: Ferrari, Franco A  
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same  
NUMBER OF SEQUENCES: 112  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Plehr, Hohbach, Teal, Albritton & Harbert  
STREET: Four Embardadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
SOFTWARE: IBM PC compatible  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477.509B  
FILING DATE: 05/08/1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 435,1993  
CLASSIFICATION: 435,1993  
APPLICATION NUMBER: US 08/175,155  
PRIORITY APPLICATION DATA: 1993  
APPLICATION NUMBER: US 08/053,049  
FILING DATE: 22-APR-1993

MOLECULE TYPE: peptide  
US-08-164-618-1  
Query Match 0.8% Score 6: DB 1: Length 15:  
Best Local Similarity 100.0% Pred No. 36:  
Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
QY 258 AAKLE 263  
DB 3 AAKLE 8

RESULT 49  
US-08-156-552A-6  
Sequence 6: Application US/08156552A  
Patent No. 576155  
GENERAL INFORMATION:  
APPLICANT: Bokoch, Gary M  
TITLE OF INVENTION: COMPOSITION OF OXIDATIVE BURST USING  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Fire Sciences Research Institute, Office of  
STREET: 10666 No. 576155th Torey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
SOFTWARE: IBM PC compatible  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/156.552A  
FILING DATE: 02-AUG-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 02-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Gerson, Edward G.  
REGISTRATION NUMBER: 31,950  
TELEPHONE: (312) 616-5400  
TELEFAX: (312) 616-5460  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

PRIOR APPLICATION DATA:  
FILING DATE: 07/11/14.618  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 06/927,258  
FILING DATE: 08-NOV-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Treacartin, Richard F.  
REGISTRATION NUMBER: 31,801  
TELEPHONE: (415) 398-3449  
TELEFAX: 415-398-3449  
INFORMATION FOR SEQ ID NO: 112:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDNESS: single  
TOPOLOGY: linear  
US-08-477-509B-112

Query Match 0.8% Score 6: DB 1: Length 21:  
Best Local Similarity 100.0% Pred No. 50:  
Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
QY 523 DPMFY 528  
DB 1 DPMFY 6

Search completed: April 6, 2001, 16:56:59  
Job time: 133 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OR protein - protein search, using sw model

Run on: April 6, 2001, 16:53:21; Search time 19.91 seconds

1212 497 Million cell updates/sec

Title: US-08-403-803-2\_COPY\_45\_750

Sequence: 1 SSNENITPRHNMARLDE.....QIYMAFVQMAATLSVFA 706

Scoring table: OLIGO

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Searched: 268465 seqs, 34193795 residues

Word size: 6

Total number of hits satisfying chosen parameters: 1505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

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3: /SID1/gcgdata/geneseq/genesep/AA1982.DAT.\*  
4: /SID1/gcgdata/geneseq/genesep/AA1983.DAT.\*  
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14: /SID1/gcgdata/geneseq/genesep/AA1993.DAT.\*  
15: /SID1/gcgdata/geneseq/genesep/AA1994.DAT.\*  
16: /SID1/gcgdata/geneseq/genesep/AA1995.DAT.\*  
17: /SID1/gcgdata/geneseq/genesep/AA1996.DAT.\*  
18: /SID1/gcgdata/geneseq/genesep/AA1998.DAT.\*  
19: /SID1/gcgdata/geneseq/genesep/AA1999.DAT.\*  
20: /SID1/gcgdata/geneseq/genesep/AA2000.DAT.\*  
21: /SID1/gcgdata/geneseq/genesep/AA2001.DAT.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the observed score, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	706	100.0	707	19	MA3852
2	706	100.0	711	21	MA3857
3	706	100.0	711	21	MA3857
4	706	100.0	750	20	Y41074
5	706	100.0	750	21	Y92619
6	706	100.0	750	21	Y92642
7	698	98.9	750	21	Y92627
8	698	98.9	750	21	Y92627
9	693	98.2	693	21	Y92666
10	685	97.0	751	18	M11524
11	658	93.2	750	17	M02234
12	643	91.1	750	21	Y92634
13	643	91.1	750	21	Y92630
14	629	89.1	750	21	Y92641
15	629	89.1	750	21	Y92641
16	629	89.1	750	21	Y92641
17	629	89.1	750	21	Y92641
18	561	79.5	750	21	Y92639
19	561	79.5	750	21	Y92640
20	524	74.2	750	21	Y92638
21	524	74.2	750	21	Y92638
22	443	62.7	693	21	Y92649
23	443	62.7	750	21	Y92646
24	431	61.0	750	21	Y92639
25	429	60.8	750	21	Y92638
26	429	60.8	750	21	Y92638
27	398	56.4	750	21	Y92631
28	375	53.1	693	21	Y92648
29	375	53.1	750	21	Y92648
30	375	53.1	750	21	Y92648
31	289	40.9	750	21	Y92644
32	289	40.9	750	21	Y92644
33	289	40.9	750	21	Y92644
34	289	40.9	750	21	Y92644
35	289	40.9	750	21	Y92644
36	289	40.9	750	21	Y92644
37	289	40.9	750	21	Y92644
38	289	40.9	750	21	Y92644
39	289	40.9	750	21	Y92644
40	289	40.9	750	21	Y92644
41	289	40.9	750	21	Y92644

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348	6	0.8	135	11	M69065	Human	flt-3 receptor
349	6	0.8	135	19	M69066	Human	flt-3 receptor
350	6	0.8	135	19	M69067	Human	flt-3 receptor
351	6	0.8	135	19	M69047	Human	flt-3 receptor
352	6	0.8	155	19	M69059	Human	flt-3 receptor
353	6	0.8	155	19	M69061	Human	flt-3 receptor
354	6	0.8	155	19	M69062	Human	flt-3 receptor
355	6	0.8	155	19	M69063	Human	flt-3 receptor
356	6	0.8	185	19	M69044	Human	flt-3 receptor
357	6	0.8	157	17	RYR1C1	Caenorhabditis elegans	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
358	6	0.8	157	17	R881.21	Caenorhabditis elegans	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
359	6	0.8	181	19	M77356	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
360	6	0.8	181	19	M77356	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
361	6	0.8	161	19	M69060	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
362	6	0.8	163	21	V15501	Neisseria meningitidis	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
363	6	0.8	166	20	T272.22	Neisseria meningitidis	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
364	6	0.8	166	20	T272.22	Neisseria meningitidis	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
365	6	0.8	169	19	V11037	H. pylori	ORF homologous to human
366	6	0.8	170	19	M69119	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
367	6	0.8	170	19	M69119	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
368	6	0.8	170	19	M69119	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
369	6	0.8	170	19	M69120	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
370	6	0.8	170	19	M69122	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
371	6	0.8	170	19	M69123	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
372	6	0.8	170	19	M69124	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
373	6	0.8	170	19	M69125	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
374	6	0.8	170	19	M69126	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
375	6	0.8	170	19	M69127	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
376	6	0.8	170	19	M69128	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
377	6	0.8	170	19	M69129	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
378	6	0.8	170	19	M69130	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
379	6	0.8	170	19	M69131	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
380	6	0.8	170	19	M69132	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
381	6	0.8	170	19	M69133	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
382	6	0.8	170	19	M69134	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
383	6	0.8	170	19	M69135	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
384	6	0.8	170	19	M69136	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
385	6	0.8	170	19	M69137	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
386	6	0.8	170	19	M69138	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
387	6	0.8	170	19	M69139	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
388	6	0.8	170	19	M69140	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
389	6	0.8	170	19	M69141	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
390	6	0.8	170	19	M69142	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
391	6	0.8	170	19	M69143	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
392	6	0.8	170	19	M69144	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
393	6	0.8	170	19	M69145	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
394	6	0.8	170	19	M69146	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
395	6	0.8	170	19	M69147	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
396	6	0.8	170	19	M69148	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
397	6	0.8	170	19	M69149	Human	Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> receptor
398	6	0.8	170	19	M69150	Human	Ca <sup>2+</sup> release

[illegible]

500	150	6	0.8	156	15	R65510	Recombinant apoA2
499	451	6	0.8	156	15	R65512	Recombinant apoA2
498	452	6	0.8	156	15	R65513	Recombinant apoA2
497	453	6	0.8	156	15	R65514	Recombinant apoA2
496	454	6	0.8	156	16	R77875	ApoA2/JR1
495	455	6	0.8	156	17	M05054	ApoA2/JR1
494	456	6	0.8	156	17	M05055	ApoA2/JR1
493	457	6	0.8	156	17	M05056	ApoA2/JR1
492	458	6	0.8	156	19	M59231	ApoA2/JR1
491	459	6	0.8	156	19	M59240	ApoA2/JR1
490	460	6	0.8	156	19	M59250	ApoA2/JR1
489	461	6	0.8	156	19	M59251	ApoA2/JR1
488	462	6	0.8	156	19	M59252	ApoA2/JR1
487	463	6	0.8	156	19	M59253	ApoA2/JR1
486	464	6	0.8	156	19	M59254	ApoA2/JR1
485	465	6	0.8	156	19	M59255	ApoA2/JR1
484	466	6	0.8	156	19	M59256	ApoA2/JR1
483	467	6	0.8	156	19	M59257	ApoA2/JR1
482	468	6	0.8	156	19	M59258	ApoA2/JR1
481	469	6	0.8	156	19	M59259	ApoA2/JR1
480	470	6	0.8	156	19	M59260	ApoA2/JR1
479	471	6	0.8	156	19	M59261	ApoA2/JR1
478	472	6	0.8	156	19	M59262	ApoA2/JR1
477	473	6	0.8	156	19	M59263	ApoA2/JR1
476	474	6	0.8	156	19	M59264	ApoA2/JR1
475	475	6	0.8	156	19	M59265	ApoA2/JR1
474	476	6	0.8	156	19	M59266	ApoA2/JR1
473	477	6	0.8	156	19	M59267	ApoA2/JR1
472	478	6	0.8	156	19	M59268	ApoA2/JR1
471	479	6	0.8	156	19	M59269	ApoA2/JR1
470	480	6	0.8	156	19	M59270	ApoA2/JR1
469	481	6	0.8	156	19	M59271	ApoA2/JR1
468	482	6	0.8	156	19	M59272	ApoA2/JR1
467	483	6	0.8	156	19	M59273	ApoA2/JR1
466	484	6	0.8	156	19	M59274	ApoA2/JR1
465	485	6	0.8	156	19	M59275	ApoA2/JR1
464	486	6	0.8	156	19	M59276	ApoA2/JR1
463	487	6	0.8	156	19	M59277	ApoA2/JR1
462	488	6	0.8	156	19	M59278	ApoA2/JR1
461	489	6	0.8	156	19	M59279	ApoA2/JR1
460	490	6	0.8	156	19	M59280	ApoA2/JR1
459	491	6	0.8	156	19	M59281	ApoA2/JR1
458	492	6	0.8	156	19	M59282	ApoA2/JR1
457	493	6	0.8	156	19	M59283	ApoA2/JR1
456	494	6	0.8	156	19	M59284	ApoA2/JR1
455	495	6	0.8	156	19	M59285	ApoA2/JR1
454	496	6	0.8	156	19	M59286	ApoA2/JR1
453	497	6	0.8	156	19	M59287	ApoA2/JR1
452	498	6	0.8	156	19	M59288	ApoA2/JR1
451	499	6	0.8	156	19	M59289	ApoA2/JR1
450	500	6	0.8	156	19	M59290	ApoA2/JR1

5501	6	0	0	8	285	1	Y79516	Soybean glutathione
5502	6	0	0	8	285	2	U57842	Human cytochrome
5503	6	0	0	8	285	3	U57842	Human cytochrome
5504	6	0	0	8	232	1	U75021	Human secreted pro-
5505	6	0	0	8	235	1	U67541	Human filic-3 ligand
5506	6	0	0	8	235	2	U67541	Human filic-3 ligand
5507	6	0	0	8	235	3	U67541	Human filic-3 ligand
5508	6	0	0	8	235	4	U67541	Human filic-3 ligand
5509	6	0	0	8	241	20	U38720	Full length wild
5510	6	0	0	8	242	19	U38720	Human cycloleucine
5511	6	0	0	8	242	20	U38720	Human cycloleucine
5512	6	0	0	8	242	21	U38720	Extended human se-
5513	6	0	0	8	242	22	U38720	Chlamydia pneumo-
5514	6	0	0	8	245	14	R36769	Human bone morpho-
5515	6	0	0	8	250	12	R36769	Factor X-LACI h9b25
5516	6	0	0	8	250	13	R36769	Human secreted pro-
5517	6	0	0	8	252	20	U34442	Chlamydia pneumo-
5518	6	0	0	8	263	19	U69469	Protein S80 ID NO
5519	6	0	0	8	265	19	U69469	Human secreted pro-
5520	6	0	0	8	270	13	R27486	Human secreted pro-
5521	6	0	0	8	270	14	R27486	Human secreted pro-
5522	6	0	0	8	270	20	U34555	Polyomavirus glan-
5523	6	0	0	8	271	19	U683300	Polyomavirus glan-
5524	6	0	0	8	271	20	U683300	Human filic-3 ligand
5525	6	0	0	8	271	21	U683300	Human filic-3 ligand
5526	6	0	0	8	276	18	U202776	Human secreted pro-
5527	6	0	0	8	276	20	U202776	Human secreted pro-
5528	6	0	0	8	277	21	U57906	Human transmembran-
5529	6	0	0	8	278	12	R87355	Human secreted pro-
5530	6	0	0	8	278	13	R87355	Human secreted pro-
5531	6	0	0	8	278	19	U74863	Human secreted pro-
5532	6	0	0	8	278	19	U74863	Human secreted pro-
5533	6	0	0	8	278	20	U74863	Human secreted pro-
5534	6	0	0	8	280	21	U51827	Human secreted pro-
5535	6	0	0	8	280	22	U51827	Human secreted pro-
5536	6	0	0	8	281	19	U683268	Human filic-3 ligand
5537	6	0	0	8	281	19	U683268	Human filic-3 ligand
5538	6	0	0	8	281	20	U683268	Human filic-3 ligand
5539	6	0	0	8	281	21	U683268	Human filic-3 ligand
5540	6	0	0	8	281	22	U683268	Human filic-3 ligand
5541	6	0	0	8	281	19	U77931	Human secreted pro-
5542	6	0	0	8	285	20	U70110	Human secreted pro-
5543	6	0	0	8	286	19	U683303	Human filic-3 ligand
5544	6	0	0	8	286	20	U683303	Human filic-3 ligand
5545	6	0	0	8	286	19	U683303	Human filic-3 ligand
5546	6	0	0	8	286	20	U683303	Human filic-3 ligand
5547	6	0	0	8	286	21	U683303	Human filic-3 ligand
5548	6	0	0	8	286	22	U683303	Human filic-3 ligand
5549	6	0	0	8	286	20	U34426	Human secreted pro-
5550	6	0	0	8	287	19	U683265	Human secreted pro-
5551	6	0	0	8	287	18	U20285	Human secreted pro-





756	6	0.8	364	19	W78085	P131L (65/66 break
757	6	0.8	364	19	W78086	P131L (98/99 break
758	6	0.8	364	19	W78087	G-CSF/IG2B/P131L
759	6	0.8	364	19	W78088	P131L (39/40 break
760	6	0.8	364	20	Y35005	Chlamydia pneumonia
761	6	0.8	364	21	Y35006	Human cycloolefin
762	6	0.8	365	11	W78091	P131L/IG2B/G-CSF
763	6	0.8	365	11	W78092	Sequence rearrange
764	6	0.8	367	19	W78114	Mutase aerotoliner
765	6	0.8	370	13	R61693	P131L/IG2B/G-CSF
766	6	0.8	370	13	R61694	P131L/IG2B/G-CSF
767	6	0.8	370	13	R61695	P131L/IG2B/G-CSF
768	6	0.8	370	13	R61696	Chemical G-CSF-P13
769	6	0.8	370	13	R61697	Chemical G-CSF-P13
770	6	0.8	370	13	R61698	P131L (35/36 break
771	6	0.8	370	13	R61699	P131L (35/36 break
772	6	0.8	370	13	R61700	P131L (35/36 break
773	6	0.8	370	13	R61701	P131L (35/36 break
774	6	0.8	370	13	R61702	P131L (35/36 break
775	6	0.8	370	13	R61703	P131L (35/36 break
776	6	0.8	370	13	R61704	P131L (35/36 break
777	6	0.8	370	13	R61705	P131L (35/36 break
778	6	0.8	370	13	R61706	P131L (35/36 break
779	6	0.8	370	13	R61707	P131L (35/36 break
780	6	0.8	370	13	R61708	P131L (35/36 break
781	6	0.8	370	13	R61709	P131L (35/36 break
782	6	0.8	370	13	R61710	P131L (35/36 break
783	6	0.8	370	13	R61711	P131L (35/36 break
784	6	0.8	370	13	R61712	P131L (35/36 break
785	6	0.8	370	13	R61713	P131L (35/36 break
786	6	0.8	370	13	R61714	P131L (35/36 break
787	6	0.8	370	13	R61715	P131L (35/36 break
788	6	0.8	370	13	R61716	P131L (35/36 break
789	6	0.8	370	13	R61717	P131L (35/36 break
790	6	0.8	370	13	R61718	P131L (35/36 break
791	6	0.8	370	13	R61719	P131L (35/36 break
792	6	0.8	370	13	R61720	P131L (35/36 break
793	6	0.8	370	13	R61721	P131L (35/36 break
794	6	0.8	370	13	R61722	P131L (35/36 break
795	6	0.8	370	13	R61723	P131L (35/36 break
796	6	0.8	370	13	R61724	P131L (35/36 break
797	6	0.8	370	13	R61725	P131L (35/36 break
798	6	0.8	370	13	R61726	P131L (35/36 break
799	6	0.8	370	13	R61727	P131L (35/36 break
800	6	0.8	370	13	R61728	P131L (35/36 break
801	6	0.8	370	13	R61729	P131L (35/36 break
802	6	0.8	370	13	R61730	P131L (35/36 break
803	6	0.8	370	13	R61731	P131L (35/36 break
804	6	0.8	370	13	R61732	P131L (35/36 break
805	6	0.8	370	13	R61733	P131L (35/36 break
806	6	0.8	370	13	R61734	P131L (35/36 break

807	6	0.8	378	19	W78097	P131L/IG2B/G-CSF
808	6	0.8	378	19	W78098	P131L/IG2B/G-CSF
809	6	0.8	378	19	W78099	P131L/IG2B/G-CSF
810	6	0.8	378	21	Y35328	Neisseria gonorrhoe
811	6	0.8	378	21	Y35329	Neisseria meningit
812	6	0.8	384	19	W78101	Chemical receptor
813	6	0.8	384	19	W78102	Chemical receptor
814	6	0.8	384	19	W78103	Chemical receptor
815	6	0.8	384	19	W78104	Chemical receptor
816	6	0.8	384	19	W78105	Chemical receptor
817	6	0.8	384	19	W78106	Chemical receptor
818	6	0.8	384	19	W78107	Chemical receptor
819	6	0.8	384	19	W78108	Chemical receptor
820	6	0.8	384	19	W78109	Chemical receptor
821	6	0.8	384	19	W78110	Chemical receptor
822	6	0.8	384	19	W78111	Chemical receptor
823	6	0.8	384	19	W78112	Chemical receptor
824	6	0.8	384	19	W78113	Chemical receptor
825	6	0.8	384	19	W78114	Chemical receptor
826	6	0.8	384	19	W78115	Chemical receptor
827	6	0.8	384	19	W78116	Chemical receptor
828	6	0.8	384	19	W78117	Chemical receptor
829	6	0.8	384	19	W78118	Chemical receptor
830	6	0.8	384	19	W78119	Chemical receptor
831	6	0.8	384	19	W78120	Chemical receptor
832	6	0.8	384	19	W78121	Chemical receptor
833	6	0.8	384	19	W78122	Chemical receptor
834	6	0.8	384	19	W78123	Chemical receptor
835	6	0.8	384	19	W78124	Chemical receptor
836	6	0.8	384	19	W78125	Chemical receptor
837	6	0.8	384	19	W78126	Chemical receptor
838	6	0.8	384	19	W78127	Chemical receptor
839	6	0.8	384	19	W78128	Chemical receptor
840	6	0.8	384	19	W78129	Chemical receptor
841	6	0.8	384	19	W78130	Chemical receptor
842	6	0.8	384	19	W78131	Chemical receptor
843	6	0.8	384	19	W78132	Chemical receptor
844	6	0.8	384	19	W78133	Chemical receptor
845	6	0.8	384	19	W78134	Chemical receptor
846	6	0.8	384	19	W78135	Chemical receptor
847	6	0.8	384	19	W78136	Chemical receptor
848	6	0.8	384	19	W78137	Chemical receptor
849	6	0.8	384	19	W78138	Chemical receptor
850	6	0.8	384	19	W78139	Chemical receptor
851	6	0.8	384	19	W78140	Chemical receptor
852	6	0.8	384	19	W78141	Chemical receptor
853	6	0.8	384	19	W78142	Chemical receptor
854	6	0.8	384	19	W78143	Chemical receptor
855	6	0.8	384	19	W78144	Chemical receptor
856	6	0.8	384	19	W78145	Chemical receptor
857	6	0.8	384	19	W78146	Chemical receptor

858	6	0.8	433	19	W72012	HSV-2 strain SB5 C
859	6	0.8	433	20	W72013	HSV-2 strain SB5 C
860	6	0.8	433	20	W72014	HSV-2 strain SB5 C
861	6	0.8	433	20	W72015	HSV-2 strain SB5 C
862	6	0.8	433	20	W72016	HSV-2 strain SB5 C
863	6	0.8	433	20	W72017	HSV-2 strain SB5 C
864	6	0.8	433	20	W72018	HSV-2 strain SB5 C
865	6	0.8	433	20	W72019	HSV-2 strain SB5 C
866	6	0.8	433	20	W72020	HSV-2 strain SB5 C
867	6	0.8	433	20	W72021	HSV-2 strain SB5 C
868	6	0.8	433	20	W72022	HSV-2 strain SB5 C
869	6	0.8	433	20	W72023	HSV-2 strain SB5 C
870	6	0.8	433	20	W72024	HSV-2 strain SB5 C
871	6	0.8	433	20	W72025	HSV-2 strain SB5 C
872	6	0.8	433	20	W72026	HSV-2 strain SB5 C
873	6	0.8	433	20	W72027	HSV-2 strain SB5 C
874	6	0.8	433	20	W72028	HSV-2 strain SB5 C
875	6	0.8	433	20	W72029	HSV-2 strain SB5 C
876	6	0.8	433	20	W72030	HSV-2 strain SB5 C
877	6	0.8	433	20	W72031	HSV-2 strain SB5 C
878	6	0.8	433	20	W72032	HSV-2 strain SB5 C
879	6	0.8	433	20	W72033	HSV-2 strain SB5 C
880	6	0.8	433	20	W72034	HSV-2 strain SB5 C
881	6	0.8	433	20	W72035	HSV-2 strain SB5 C
882	6	0.8	433	20	W72036	HSV-2 strain SB5 C
883	6	0.8	433	20	W72037	HSV-2 strain SB5 C
884	6	0.8	433	20	W72038	HSV-2 strain SB5 C
885	6	0.8	433	20	W72039	HSV-2 strain SB5 C
886	6	0.8	433	20	W72040	HSV-2 strain SB5 C
887	6	0.8	433	20	W72041	HSV-2 strain SB5 C
888	6	0.8	433	20	W72042	HSV-2 strain SB5 C
889	6	0.8	433	20	W72043	HSV-2 strain SB5 C
890	6	0.8	433	20	W72044	HSV-2 strain SB5 C
891	6	0.8	433	20	W72045	HSV-2 strain SB5 C
892	6	0.8	433	20	W72046	HSV-2 strain SB5 C
893	6	0.8	433	20	W72047	HSV-2 strain SB5 C
894	6	0.8	433	20	W72048	HSV-2 strain SB5 C
895	6	0.8	433	20	W72049	HSV-2 strain SB5 C
896	6	0.8	433	20	W72050	HSV-2 strain SB5 C
897	6	0.8	433	20	W72051	HSV-2 strain SB5 C
898	6	0.8	433	20	W72052	HSV-2 strain SB5 C
899	6	0.8	433	20	W72053	HSV-2 strain SB5 C
900	6	0.8	433	20	W72054	HSV-2 strain SB5 C
901	6	0.8	433	20	W72055	HSV-2 strain SB5 C
902	6	0.8	433	20	W72056	HSV-2 strain SB5 C
903	6	0.8	433	20	W72057	HSV-2 strain SB5 C
904	6	0.8	433	20	W72058	HSV-2 strain SB5 C
905	6	0.8	433	20	W72059	HSV-2 strain SB5 C
906	6	0.8	433	20	W72060	HSV-2 strain SB5 C
907	6	0.8	433	20	W72061	HSV-2 strain SB5 C
908	6	0.8	433	20	W72062	HSV-2 strain SB5 C

909	6	0.8	471	20	Y00878	Sucrose fatty acid
910	6	0.8	471	20	Y00879	Pre-pro BDNF
911	6	0.8	471	20	Y00880	Thrombospondin
912	6	0.8	471	21	Y69310	Thrombospondin
913	6	0.8	472	21	Y66873	Amino acid sequencer
914	6	0.8	476	18	W53754	Human flavonoid
915	6	0.8	477	20	Y23595	Human matrix metallo
916	6	0.8	477	20	Y23596	Human matrix metallo
917	6	0.8	478	19	W63095	Yersinia enterocolitica
918	6	0.8	478	19	W63095	Yersinia enterocolitica
919	6	0.8	479	19	W44068	Schistosoma mansoni
920	6	0.8	481	20	Y10509	CD231-16.1/14
921	6	0.8	481	20	Y10509	CD231-16.1/14
922	6	0.8	484	20	Y18050	768kD protein sequen
923	6	0.8	484	20	Y18051	768kD protein sequen
924	6	0.8	487	19	W60519	Cattle Factor-Xa
925	6	0.8	487	19	W60519	Cattle Factor-Xa
926	6	0.8	488	19	W62511	Human Factor X
927	6	0.8	488	19	W76219	Human Factor X
928	6	0.8	488	19	W76219	Human Factor X
929	6	0.8	488	19	W76218	Human Factor X
930	6	0.8	488	19	W76218	Human Factor X
931	6	0.8	489	19	Y27647	Human calcium chara
932	6	0.8	489	19	W82549	Human LTR-phorb-4
933	6	0.8	490	16	Y27300	Human auxiliary c
934	6	0.8	490	16	Y27300	Human auxiliary c
935	6	0.8	490	16	Y27300	Human auxiliary c
936	6	0.8	490	16	Y27300	Human auxiliary c
937	6	0.8	490	17	Y27300	Human auxiliary c
938	6	0.8	490	17	Y27300	Human auxiliary c
939	6	0.8	490	17	Y27300	Human auxiliary c
940	6	0.8	490	17	Y27300	Human auxiliary c
941	6	0.8	490	17	Y27300	Human auxiliary c
942	6	0.8	490	17	Y27300	Human auxiliary c
943	6	0.8	490	17	Y27300	Human auxiliary c
944	6	0.8	490	17	Y27300	Human auxiliary c
945	6	0.8	490	17	Y27300	Human auxiliary c
946	6	0.8	490	17	Y27300	Human auxiliary c
947	6	0.8	490	17	Y27300	Human auxiliary c
948	6	0.8	490	17	Y27300	Human auxiliary c
949	6	0.8	490	17	Y27300	Human auxiliary c
950	6	0.8	490	17	Y27300	Human auxiliary c
951	6	0.8	490	17	Y27300	Human auxiliary c
952	6	0.8	490	17	Y27300	Human auxiliary c
953	6	0.8	490	17	Y27300	Human auxiliary c
954	6	0.8	490	17	Y27300	Human auxiliary c
955	6	0.8	490	17	Y27300	Human auxiliary c
956	6	0.8	490	17	Y27300	Human auxiliary c
957	6	0.8	490	17	Y27300	Human auxiliary c
958	6	0.8	490	17	Y27300	Human auxiliary c
959	6	0.8	490	17	Y27300	Human auxiliary c
960	6	0.8	490	17	Y27300	Human auxiliary c











173 dlyvnyarfedfktiercdmkincgsklyvayrkyvtrgkvknaqlagvaylyvgeda 232  
 189 DPAKPSYPCGKNGGVOGKNTLAKGQVTPGKAPKAYAPRGKIAEYKCS 248  
 233 dyfegvaykpsvpmppgvgvgnlnlnhgaqdp2lcpypaeyeyrrglaevy1pa1 292  
 249 PVPPTGDAQLLEKMGKAPADSSKRGSLVPPYVNGQCTONSTQVAKHSTHST 308  
 293 pvpbydydqlltemgseppdeevrgalkvrvvsgfvtgnctvkvmbhstetw 352  
 309 TRTVVGTGKAGVPEPVYVILGCHDSVWFGIDPSSGAVVHVSPTLAKKESKH 368  
 351 ttrvvtgsktgnvpevyl1ggnhdeevy1gqldqgdaevvkvstgskhsgvyp 412  
 369 RTTIFASMAEERFGLGSTEMEBSRLAQRVAYVIAHDSISGNTLVKVCPLAT 428  
 413 rttltfalsadeevy1lgseveeaeat1lqevayvadaalegny1lvdcprlmy 472  
 429 LVHNI/NTELSPDGEKGLYBSMTKSPSPGAPRIKSLGSDNDFVPPORGLAS 486  
 472 LVHNI/NTELSPDGEKGLYBSMTKSPSPGAPRIKSLGSDNDFVPPORGLAS 486  
 478 GRATTIKMETKPSGQPLVHGYETTELKPTDPRVETLVKVAQVNGVPELANT 548  
 533 grattyhmetkfpqplvhyevetvlekypdmklyplvvaqvgvntelanly 592  
 549 LPDGDVAVVAVYADVYISMKHQRKMTKVSQSPGAPRIKSLGSDNDFVPPOR 608  
 593 lpdgdvavv1rvyady1smkhqemklyvavdal1favvntelaakfcerq 652  
 609 PDSNPVTYVANNQVLTUATLPIDGLDPRPPTRRVYVPSMNTKAGSPFCTAL 668  
 653 fdnmpv1tmnqnlmterldp1gldp1rtrvlyvpsmhvypesfpqlyadl 712  
 669 PDSEKVPDSKMGEPKQIVYAAFTVQAALTESEA 706  
 713 fdlskvpdsamgvrkqlyvadt1qdaael1aeva 750

RESULT 9  
 ID Y92666 standard: Protein: 693 AA.  
 AC Y92666;  
 DC 10-AUG-2000 (first entry)  
 DE Human prostate specific membrane antigen splice variant.  
 XX Prostate specific membrane antigen splice variant: vaselation.  
 XX Cytotoxic T-lymphocyte immunity; self-protein: cancer: Breast cancer:  
 FM

PT peptide antigens for the treatment of breast and prostate cancer

XX Example 1: Page 1: 220pp: English.

CC This is a splice variant of human prostate specific membrane antigen  
 CC (PSM) (see Y92619). Immunogenic analogues of PSM can be used in the  
 CC claimed method as an adjuvant to induce a CTL response. Substant  
 CC diolymers, antibody binding regions and cysteine residues involved in  
 CC disulfide bridges of the protein are identified. The method compris  
 CC suitable for the insertion of foreign T helper epitopes were identifi  
 CC The method is used for inducing immune responses against weakly  
 CC immunogenic cell-associated peptide antigens (PA) such as those  
 CC associated with prostate cancer. The method comprises effecting  
 CC fibroblast growth factor Bb (FGFB). The method comprises effecting  
 CC simultaneous presentation by antigen producing cells (APCs) of the  
 CC animal immune system of (1) at least 1 CTL (cytotoxic T-lymphocyte)  
 CC cell-associated PA; and (2) at least 1 first T helper cell group which is  
 CC foreign to the animal. Analogues of human PSM, human Her2 and  
 CC human/murine FGFB comprising a substantial part of all known and  
 CC predicted CTL and B cell epitopes of the respective PA and including at  
 CC least one foreign T helper epitope are used to treat prostate, prostate  
 CC PSM, FGFB and Her2, respectively.

XX Sequence 693 AA:  
 DB

Query Match 98.7%; Score 693; DB 21; Length 693;  
 Heat Local similarity 100.0%; Pred No. of  
 Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 14 HKAFIDELAKENIKFVNFPIHACTGBOFQALNKGQSKFQSLVSEIARIVL 73  
 DB 1 MKAFIDELAKENIKFVNFPIHACTGBOFQALNKGQSKFQSLVSEIARIVL 60  
 DB 74 SYPTAPVYISIKENKNTFNTSLFPPPGCEVNSDVPFPAATSPQOQEDQVYV 133  
 DB 61 syptapvys1lknegntfntslfpppgcevad1vpfpaatspqmpedv1yv 120  
 DB 134 MKAFIDELAKENIKFVNFPIHACTGBOFQALNKGQSKFQSLVSEIARIVL 193  
 DB 121 nyatetdtkfctcdmkincsgklyvayrkyvtrgkvknaqlagvaylyvgeda 180  
 DB 194 GYVSGPSCMNPGGVQKNTLAKGQVTPGKAPKAYAPRGKIAEYKCS 253  
 DB 181 gyvsgpvm1pgvgvgnlnlnhgaqdp2lcpypaeyeyrrglaevy1pa1pa 240  
 DB 254 GYVSGPSCMNPGGVQKNTLAKGQVTPGKAPKAYAPRGKIAEYKCS 313

prostate cancer: cell-associated peptide antigen: foreign epitope.  
 XX Homo sapiens.  
 PH Key  
 PH Region  
 PH 30..51  
 PH /label=insertion\_region  
 PH /note="suitable for foreign T helper epitope insertion"  
 PH 153..173  
 PH /label=insertion\_region  
 PH /note="suitable for foreign T helper epitope insertion"  
 PH 212..232  
 PH /label=insertion\_region  
 PH /note="suitable for foreign T helper epitope insertion"  
 PH 241..267  
 PH /label=insertion\_region  
 PH /note="suitable for foreign T helper epitope insertion"  
 PH 385..408  
 PH /label=insertion\_region  
 PH /note="suitable for foreign T helper epitope insertion"  
 PH 431..457  
 PH /label=insertion\_region  
 PH /note="suitable for foreign T helper epitope insertion"  
 PH 541..573  
 PH /label=insertion\_region  
 PH /note="suitable for foreign T helper epitope insertion"  
 PH 578..605  
 PH /label=insertion\_region  
 PH /note="suitable for foreign T helper epitope insertion"  
 PH 615..642  
 PH /label=insertion\_region  
 PH /note="suitable for foreign T helper epitope insertion"

MO200020027-AZ.  
 PH 13-APR-2000.  
 PH 05-OCT-1999; 99NO-DK00525.  
 PH 05-OCT-1998; 98BK-0001261.  
 PH 20-OCT-1998; 98OS-0105921.  
 PH (MEDI-) M & E BIOTECR AS.  
 PH Steinaa L, Mouritsen S, Nielsen KG, Heaning J, Leach D, Dalum I;  
 PH Gertsen M, Birk P, Mathiasen O;  
 PH WPI: 2000-349917/30.  
 PH N-PSDB: A09454.  
 PH Inducing immune responses to weakly immunogenic, tumor associated

DB 241 gyvdaql1temgseppdeevrgalkvrvvsgfvtgnctvkvmbhstetw 300  
 DB 314 GYVDAQL1TEMGSEPPDEEVRGALKVRVVSFGFTGNTCEKVKHSTHSTHST 373  
 DB 301 yvclt1gavpedvyy1lgnhdeevy1gqldqgdaevvkvstgskhsgvyp 360  
 DB 374 PRSMDAERFGLGSTEMEBSRLAQRVAYVIAHDSISGNTLVKVCPLAT 433  
 DB 361 fawdeetck1g1gavveeaeat1lqevayvadaalegny1lvdcprlmy1vhl 430  
 DB 434 PTKELSPDGEKGLYBSMTKSPSPGAPRIKSLGSDNDFVPPORGLASGRAT 493  
 DB 421 kshkspdgscgsklyvcevkpkpdmklyvavdal1favvntelaakfcerq 480  
 DB 494 TRNMTKPSGQPLVHGYETTELKPTDPRVETLVKVAQVNGVPELANT 553  
 DB 481 kshkspdgscgsklyvcevkpkpdmklyvavdal1favvntelaakfcerq 540  
 DB 554 BDVAVVAVYADVYISMKHQRKMTKVSQSPGAPRIKSLGSDNDFVPPORGLAS 613  
 DB 541 cdgavv1rvyady1smkhqemklyvavdal1favvntelaakfcerq 600  
 DB 614 PVTGNGQVTPGKAPKAYAPRGKIAEYKCS 673  
 DB 601 pvt1mmnqnlmterldp1gldp1rtrvlyvpsmhvypesfpqlyad1fdes 660  
 DB 674 PDSNPVTYVANNQVLTUATLPIDGLDPRPPTRRVYVPSMNTKAGSPFCTAL 706  
 DB 661 kvdpkavgevk1gqlyvadt1qdaael1aeva 753

RESULT 10  
 ID M31524 standard: protein: 751 AA.  
 AC M31524;  
 DC 14-MAY-1998 (first entry)  
 DE Prostate-specific membrane antigen.  
 XX Prostate-specific membrane antigen: PSM; monoclonal antibody:  
 XX Prostate cancer; metastatic.  
 XX Homo sapiens.  
 PH Key  
 PH Protein  
 PH 58..750  
 PH /label=PSM  
 PH /note="Prostate PSM protein, a variant of PSM"

P7		/note= "putative transmembrane domain"
F7	Region	716..723
P8		Peptide selected for monoclonal antibody
F8	/note=	development.
XK	M09J35616-A1.	
PD	07-OCT-1997.	
PN	25-MAR-1997.	97NO-U0S0521d.
PF	25-MAR-1997.	96DS-06J1399.
KX	(PACI-) PACIFIC NORTHWEST CANCER FOUNO.	
PA	Boynoun AL., Holmes EH., Murphy GP., Tiao WT:	
P1	WPI; 1997-489396/45.	
D8	Monoclonal antibody against prostate-specific membrane antigen -	
PT	used for diagnosis and treatment of prostatic cancer	
P5	Claim 2; Fig 1; 76pp: English.	
CC	The present sequence represents the prostate-specific membrane antigen	
CC	(PSMA). A novel monoclonal antibody (MAB) has been developed which can	
CC	an antigen binding region specific for the extracellular domain (ECD) of	
CC	PSMA. The MAb is used for detecting the presence of PSMA (or its new	
CC	specimens or cancer cells within tissue sections stained by immunohistochemical techniques for detection of PSA levels of PSMA are elevated and	
CC	monitoring of prostate cancer, in which levels of PSA are elevated and	
CC	Rita for carrying out this method are also included within the scope of	
CC	cancer and associated diseases. The MAB may be used for treatment of prostate	
CC	toxin or radiosteoep. Mabs directed against ECD provide a more	
CC	IOD, and detects PSMA only in necrotic or apoptotic cells (and can not	
CC	without the need for a biopsy sample.	
XX	Sequence 751 AA:	
QY	Query Match	97.0%; Score 685; DB 18; Length 751;
Bt	Best Local Similarity	100.0%; Prid. No. 0;
Hatches	685; Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	<pre>22 KENIKTKLVNTOIPHLAAGTDRNQALAKAQIGGSKRGESVSELAHVDLISPKTHP 81 67 KKKNIITLYINLTGIPLHSLEGTGNGLAQKIQLGVKEFIDAVEIAVDVLISPPKHP 126</pre>	

[illegible]

PT	04-NOV-1996	(first entry)
DE		Prostate-specific membrane antigen.
EN		Prostate-specific membrane antigen; PSM; promoter; prostate cancer;
FR		metastasis; therapy; diagnosis.
OS		
OS		Homo sapiens.
XX		
XX	Key	Location/Qualifiers
XX	Domain	/label= Transmembrane_domain
PT	Modified-site	106
PT	Modified-site	/label= N-glycosylation_site
PT	Modified-site	121
PT	Modified-site	/label= N-glycosylation_site
PT	Modified-site	140
PT	Modified-site	/label= N-glycosylation_site
PT	Modified-site	153
PT	Modified-site	/label= N-glycosylation_site
PT	Modified-site	136
PT	Modified-site	/label= N-glycosylation_site
PT	Modified-site	476
PT	Modified-site	/label= N-glycosylation_site
PT	Modified-site	68
PT	Modified-site	/label= N-glycosylation_site
XX		
XX	W06926572-A1.	
XX		
PD	29-AUG-1996.	
XX		
PT	23-FEB-1996;	96NO-US024424.
PT	02-JUN-1995;	95US-04-70275.
PR	24-FEB-1995;	95US-0394152.
PR	02-JUN-1995;	95US-0466381.
XX		
XX	(SLD ) SLDN KETTERING INST CANCER RES.	
XX		
PI	Fair WR, Hesdon MDW, Israeli RS;	
XX	WPI: 1396-402365/40.	
DR	N-F50B; 750785.	
XX		
XX	DNA encoding alternatively apliced prostate-specific membrane	
PT	antigen - useful to develop prods. for detecting hematogenous	
XX	metastatic tumour cells, or prostate cancer progression	
XX		
P6	Example 1; Fig 47A-D: 284bp. English.	
XX		
XX	Prostate-specific membrane (PSM) antigen (W07234) is a type II	

[illegible]





Query Match	90.1%	Score 643	DB 21	Length 750
Heat Local Similarity	100.0%	Pred. No. 0		
Matches 643	Convertible	0	Mismatches	0
0			Indels	0
0			Gaps	0
QY	64	VELAHVAVLLVLLSLKTPHMYSTINEDCHTEFNFSTSLFEPPOCKEWNADVTPNSAFSQ	123	
DB	108	VELAHVAVLLVLLSLKTPHMYSTINEDCHTEFNFSTSLFEPPOCKEWNADVTPNSAFSQ	167	
QY	124	GHPEADLVAVNAARFEPFKLEPMKRLNCGSRKIVLVNGVRCRQNVNMLQAKVTL	183	
DB	168	GHPEADLVAVNAARFEPFKLEPMKRLNCGSRKIVLVNGVRCRQNVNMLQAKVTL	243	
QY	184	VSDPADPVKVSQVSPCKNPGCGVGNQKRLNMGADQKQVPCVGNANVREKICADN	227	
DB	228	VSDPADPVKVSQVSPCKNPGCGVGNQKRLNMGADQKQVPCVGNANVREKICADN	287	
QY	244	GLSPVHNGVGNQKRLNMGADQKQVPCVGNANVREKICADN	303	
DB	288	GLSPVHNGVGNQKRLNMGADQKQVPCVGNANVREKICADN	347	
QY	304	STNENYVNVVLTGLCAVREKIVLVNGVRCRQNVNMLQAKVTL	363	
DB	348	STNENYVNVVLTGLCAVREKIVLVNGVRCRQNVNMLQAKVTL	407	
QY	364	EGCRVREKIVLVNGVRCRQNVNMLQAKVTL	423	
DB	408	EGCRVREKIVLVNGVRCRQNVNMLQAKVTL	467	
QY	424	PLATSLVHMLKTELSPDGCRCSTLSEMTATKPPSPFQPMRPIKSLGCDVPEPKR	483	
DB	468	PLATSLVHMLKTELSPDGCRCSTLSEMTATKPPSPFQPMRPIKSLGCDVPEPKR	537	
QY	484	LCATGACAVYVHMLKTELSPDGCRCSTLSEMTATKPPSPFQPMRPIKSLGCDVPEPKR	543	
DB	528	LCATGACAVYVHMLKTELSPDGCRCSTLSEMTATKPPSPFQPMRPIKSLGCDVPEPKR	587	
QY	544	ANSTVLPDGCRCSTLSEMTATKPPSPFQPMRPIKSLGCDVPEPKR	603	
DB	588	ANSTVLPDGCRCSTLSEMTATKPPSPFQPMRPIKSLGCDVPEPKR	647	
QY	604	ERLADPNSNVVLTGLCAVREKIVLVNGVRCRQNVNMLQAKVTL	663	
DB	648	ERLADPNSNVVLTGLCAVREKIVLVNGVRCRQNVNMLQAKVTL	707	
QY	664	LYDAFLPDSNVVLTGLCAVREKIVLVNGVRCRQNVNMLQAKVTL	706	
DB	708	LYDAFLPDSNVVLTGLCAVREKIVLVNGVRCRQNVNMLQAKVTL	750	

ID	** Y92630 standard; Protein: 750 AA.
XX	
XX	Y92630;
AC	
KC	
NC	
DC	
EC	10-AGO-2000 (first entry)
DE	
DB	Mutant human prostate specific membrane antigen construct, NP8M10.1.
DM	
DN	Prostate specific membrane antigen immunogenized construct; mutant:
NM	waltonite; cytochrome c complexed immunogenized peptide antigen; foreign epitope.
FM	prostate cancer; cell-associated peptide antigen; foreign epitope.
IM	
CC	
CS	Homo sapiens.
OS	Synthetic.
XX	
FH	
FI	Key
FT	Location/Qualifiers
FT	Peptide
FT	21..41
FT	/label= P30
FT	/accession= Foreign epitope*
FT	674..688
FT	Peptide
FT	/label= P2
FT	/note= Foreign epitope*
MO	MO2000020027.A2
PD	
PD	13-Apr-2000.
PR	
PR	05-OCT-1999; 99MC-DK00525.
XX	
XX	05-OCT-1999; 98OR-0001261.
PR	20-OCT-1999; 98MS-0105011.
XX	
XX	(MED-) M & E BIOCHEM AB.
P1	
P1	Stetina L, Mouritzen S, Nielsen KG, Haaning J, Leach D, Dalum I:
P1	Gautam A, Birx P, Karlsson G;
P1	WPI, 2000-349917/30.
PT	
PT	Inducing immune responses to weakly immunogenic, tumor associated
PT	peptide antigens for the treatment of breast and prostate cancer
XX	
XX	Example 1; Page -1; 220pp; English.
CC	
XX	Y92627-49 are mutant immunogenized human prostate specific membrane
CC	antigen (PSM) constructs, which contain foreign epitopes (P2 and/or P30)
CC	antigenic peptides. The method of PSM can be used in the claimed method as an
CC	immunogenized antigenic peptide. The method of PSM can be used in the
CC	binding regions and cysteine residues involved in disulfide bonds are
CC	preserved in the immunogenized forms. The method is used for inducing

immunoreactive against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (self-protein), e.g., carcinoembryonic antigen (CEA), alpha-fetoprotein (AFP), and/or fibroblast growth factor-8b (FGF8b). The PA were prepared by a sequential immunization protocol [1] using a mixture of CEA, AFP, and/or simultaneous presentation by antigen producing cells (APCs) of the same immunogen system of (1) at least 1 CTL cytotoxic T lymphocyte (CTL)-associated PA; and (2) another self-antigenic PA which is foreign to the animal. Analogues of human PSM, human HcR2 and human/murine FGF8b comprising a substantial part of all known and predicted amino acid sequences of the respective PA and including at least one foreign T cell epitope were used as immunogens. In addition, CC to treat prostate, prostate/breast or breast cancer when the PA is human PSM, FGF8b and HcR2, respectively.

CC PMV, FGF8b and HcR2, respectively.

(979619), which appears on pages 164-167 of the specification.

Sequence 750 AA:

[illegible]

Query Match	Best Local Similarity	89.1%: Pared 63%: DB 21: Length 750:
Matches 63%: Corrective 0%: Mismatches 0%: Indels 0%: Gaps 0%:		
0Y	1 SENEVETPNNMAALDELEMANIKKFFVIFPCPLAGCBOGNOALQISOMENCG	60
DB	45 SENEETLIPHPMAALDELEMANIKKFFVIFPCPLAGCBOGNOALQISOMENCG	104
0Y	45 LDEVELANEDVLLSPKTHNYRTSITNEGCEKFPSTSEPEPPCEVENDVPPSSAF	120
DB	105 LDEVELANEDVLLSPKTHNYRTSITNEGCEKFPSTSEPEPPCEVENDVPPSSAF	160
0Y	121 SPQCPKAPDLYVNNATKPRFLEMDKINSCKITVATKPRGKNNQMLQALAC	180
DB	165 SPQCPKAPDLYVNNATKPRFLEMDKINSCKITVATKPRGKNNQMLQALAC	224
0Y	181 VLYSDADYAVCAVSPEDNNIDCCOVRNNLNLNMQADPPPTPQVMEATFAGCA	240
DB	225 VLYSDADYAVCAVSPEDNNIDCCOVRNNLNLNMQADPPPTPQVMEATFAGCA	304
0Y	241 EAVGSEIVPHTGIDAKLETKGCAAPPSKSSLEVPYVNGTPTGSEVSTVPM	280
DB	285 EAVGSEIVPHTGIDAKLETKGCAAPPSKSSLEVPYVNGTPTGSEVSTVPM	344
0Y	301 HHSNENETRYVYGLKAGKAPPPVYVLSGHDSMRFQIGDSQAMVHYETVRFCT	360
DB	345 HHSNENETRYVYGLKAGKAPPPVYVLSGHDSMRFQIGDSQAMVHYETVRFCT	400
0Y	361 LKKEQNPPTLITFSLMAKQFLEKQVDEYVLSGHDSMRFQIGVYVNNQSTQVTR	420
DB	405 LKKEVNPPTLITFSLMAKQFLEKQVDEYVLSGHDSMRFQIGVYVNNQSTQVTR	464

ID	Y93641 standard; protein; 750 AA.
AC	Y93641.
DE	
DT	10-AUG-2000 (first entry)
DE	Mutant human prostate specific membrane antigen construct, hPSM10.0.
DE	Prostate specific membrane antigen; immunogenized construct; mutant;
FW	vaccination; cyclocock T lymphocyte immunity; breast cancer;
FW	prostate cancer; cell-associated peptide antigen; foreign epitope.
KA	
OS	Human sapientia.
OS	Synthetic.
XX	
XX	Key
FT	Peptide
FT	Location/Qualifiers
FT	/label="p2
FT	/note="foreign epitope"
XX	
XX	W0200020027-A2.
XD	13-APR-2000.
XX	
XX	05-OCT-1999; 99MO-DR00325.
XX	
XX	05-OCT-1998; 98DK-0001261.
PR	20-OCT-1998; 98DS-0105011.
XX	
XX	(MEB1-) M & E BIOTECN AS.
XX	
XX	

PI Steinae L., Mouritsen S., Nielsen KG., Haaning J., Leach D., Dalum I.  
 PI Gautam A., Birk P., Karlsson G.  
 WPI: 2000-349317/30.  
 PT Inducing immune responses to weakly immunogenic, tumor associated  
 PT peptide antigens for the treatment of breast and prostate cancer  
 Example 1: Page -1: 220pp: English.

CC Y92627-49 are mutant immunogenized human prostate specific membrane  
 CC antigen (PSM) constructs, which contain foreign epitopes (P2 and/or P30).  
 CC The PSM constructs are immunized into mice by subcutaneous injection of  
 CC adjuvanted to induce a CTL response. Subdominant CTL epitopes, antibody  
 CC binding regions and cysteine residues involved in disulfide bonds are  
 CC preserved in the immunogenized forms. The method is used for inducing  
 CC immune responses against weakly immunogenic cell-associated peptide  
 CC antigens. The method is used for inducing immune responses against  
 CC human prostate specific membrane antigen (PSM), heregulin 2 (Hc2) and/or  
 CC fibroblast growth factor 8b (FGF8b). The method comprises effecting  
 CC simultaneous presentation by antigen producing cells (APCs) of the  
 CC antigen immun system of: (1) at least 1 CTL (cytotoxic T-lymphocyte)  
 CC cell-associated P2; and (2) at least 1 first T helper cell group which is  
 CC foreign to the animal. Analogues of human PSM, human Hc2 and  
 CC human/murine FGF8b comprising a substantial part of all known and  
 CC predicted human/murine PSM, human Hc2 and human/murine FGF8b  
 CC to treat prostate, prostate/breast or breast cancer when the P2 is human  
 CC PSM, FGF8b and Hc2, respectively.  
 CC Note: This sequence was constructed from the wild type human PSM  
 CC (Y92633), which appears on pages 164-167 of the specification.  
 XX Sequence 750 AA:

Query Match 89.1%; Score 629; DB 21; Length 750;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 629; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SENEATNPNNHKAFLDELAENKIFKLYNPQIPHLACFQNPOLAKOISQKFEK 60  
 QY 45 SENEATNPNNHKAFLDELAENKIFKLYNPQIPHLACFQNPOLAKOISQKFEK 104  
 QY 61 LQVATLANTDILSPNKTNPRTISLIMDCHEZFNLSLEPPPCRENDVYPPSPAF 120  
 QY 105 LQVATLANTDILSPNKTNPRTISLIMDCHEZFNLSLEPPPCRENDVYPPSPAF 164  
 QY 121 SPOQMBSDLYVYVARTEDFPLEDMKNTKNGSKIVATKAKVKNQKNAQALAKG 180  
 QY 165 SPOQMBSDLYVYVARTEDFPLEDMKNTKNGSKIVATKAKVKNQKNAQALAKG 224

QY 181 VTIYSDPADYPAKCVKSPYDQKNDLPGCGVGNKILNLMKAGDPLFPGYPAKNAEIRKIA 240  
 DB 225 VTIYSDPADYPAKCVKSPYDQKNDLPGCGVGNKILNLMKAGDPLFPGYPAKNAEIRKIA 284  
 QY 241 EAVGLPSIPVHPICGYDAKLEKNGSAPDSSNKGSLKVPYWGPGFQNPFSNQGVRN 300  
 DB 265 EAVGLPSIPVHPICGYDAKLEKNGSAPDSSNKGSLKVPYWGPGFQNPFSNQGVRN 344  
 QY 301 HINSTNEVTRIVYIGTLKCAVDPDRVYLGGHBSWFGIDPQSGAAVHETVSPGT 360  
 DB 345 HINSTNEVTRIVYIGTLKCAVDPDRVYLGGHBSWFGIDPQSGAAVHETVSPGT 404  
 QY 361 LKFGCHRRPRTILPASHDAEFVGLGSTDAENRSLQERGVATINDGSIKONTYLV 420  
 DB 405 LKFGCHRRPRTILPASHDAEFVGLGSTDAENRSLQERGVATINDGSIKONTYLV 464  
 QY 421 DCPYLVATLNLKTELSKSPDPCFSGSLSEKFTKSPGPPGQMRISLIGSNDPFGY 480  
 DB 465 DCPYLVATLNLKTELSKSPDPCFSGSLSEKFTKSPGPPGQMRISLIGSNDPFGY 524  
 QY 481 RORLCILSGNAVYVWVWVNSGCPRLVSVYVETVYKFDPMKXVYVYVQVPGGV 540  
 DB 525 RORLCILSGNAVYVWVWVNSGCPRLVSVYVETVYKFDPMKXVYVYVQVPGGV 584  
 QY 541 PEANSLVLPFCRDVYVYVLRNKAADITSISNKHQDPTVCGSPDSISNKNKPEAS 600  
 DB 585 PEANSLVLPFCRDVYVYVLRNKAADITSISNKHQDPTVCGSPDSISNKNKPEAS 644  
 QY 601 KFSBRLODPKSNRIVLBNKQDLKPLRN 628  
 DB 645 KFSBRLODPKSNRIVLBNKQDLKPLRN 673

RESULT 16  
 Y92633 standard: Protein: 750 AA.  
 XX Y92633:  
 AC Y92633:  
 XX 10-NOV-2000 (first entry)  
 DE Mutant human prostate specific membrane antigen construct, hPSM.10.  
 XX Prostate specific membrane antigen; immunogenized construct; mutant;  
 XX vaccination; cytotoxic T-lymphocyte immunity; breast cancer;  
 KW prostate cancer; cell-associated peptide antigen; foreign epitope.  
 XX Homo sapiens.  
 XX Synthetic.  
 XX

PI Key Location/Qualifiers  
 PI Peptide 24-38  
 PI /label=P2  
 PI /label=foreign epitope\*  
 PI /label=P30  
 PI /label=P30  
 PI /note="foreign epitope"  
 PT W0200020027-X2.  
 PD 13-APR-2000.  
 PD 05-OCT-1999: 99NO-DB00525.  
 PD 05-OCT-1998: 98DK-0001261.  
 PD 20-OCT-1998: 98US-0105011.  
 PX (HBT-1) M & B BIOTECH AS.  
 PX Steinae L., Mouritsen S., Nielsen KG., Haaning J., Leach D., Dalum I.  
 PX Gautam A., Birk P., Karlsson G.  
 PX WPI: 2000-349317/30.  
 PT Inducing immune responses to weakly immunogenic, tumor associated  
 PT peptide antigens for the treatment of breast and prostate cancer  
 Example 1: Page -1: 220pp: English.

XX Y92627-49 are mutant immunogenized human prostate specific membrane  
 XX antigen (PSM) constructs, which contain foreign epitopes (P2 and/or P30).  
 XX The PSM constructs are immunized into mice by subcutaneous injection of  
 XX adjuvanted to induce a CTL response. Subdominant CTL epitopes, antibody  
 XX binding regions and cysteine residues involved in disulfide bonds are  
 XX preserved in the immunogenized forms. The method is used for inducing  
 XX immune responses against weakly immunogenic cell-associated peptide  
 XX antigens. The method is used for inducing immune responses against  
 XX human prostate specific membrane antigen (PSM), heregulin 2 (Hc2) and/or  
 XX fibroblast growth factor 8b (FGF8b). The method comprises effecting  
 XX simultaneous presentation by antigen producing cells (APCs) of the  
 XX antigen immun system of: (1) at least 1 CTL (cytotoxic T-lymphocyte)  
 XX cell-associated P2; and (2) at least 1 first T helper cell group which is  
 XX foreign to the animal. Analogues of human PSM, human Hc2 and  
 XX human/murine FGF8b comprising a substantial part of all known and  
 XX predicted human/murine PSM, human Hc2 and human/murine FGF8b  
 XX to treat prostate, prostate/breast or breast cancer when the P2 is human  
 XX PSM, FGF8b and Hc2, respectively.  
 XX Note: This sequence was constructed from the wild type human PSM  
 XX (Y92633), which appears on pages 164-167 of the specification.  
 CC

Query Match 89.0%; Score 628; DB 21; Length 750;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 628; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SENEATNPNNHKAFLDELAENKIFKLYNPQIPHLACFQNPOLAKOISQKFEK 60  
 DB 45 SENEATNPNNHKAFLDELAENKIFKLYNPQIPHLACFQNPOLAKOISQKFEK 104  
 QY 61 LQVATLANTDILSPNKTNPRTISLIMDCHEZFNLSLEPPPCRENDVYPPSPAF 120  
 DB 105 LQVATLANTDILSPNKTNPRTISLIMDCHEZFNLSLEPPPCRENDVYPPSPAF 164  
 QY 121 SPOQMBSDLYVYVARTEDFPLEDMKNTKNGSKIVATKAKVKNQKNAQALAKG 180  
 DB 165 SPOQMBSDLYVYVARTEDFPLEDMKNTKNGSKIVATKAKVKNQKNAQALAKG 224  
 QY 181 VTIYSDPADYPAKCVKSPYDQKNDLPGCGVGNKILNLMKAGDPLFPGYPAKNAEIRKIA 240  
 DB 225 VTIYSDPADYPAKCVKSPYDQKNDLPGCGVGNKILNLMKAGDPLFPGYPAKNAEIRKIA 284  
 QY 241 EAVGLPSIPVHPICGYDAKLEKNGSAPDSSNKGSLKVPYWGPGFQNPFSNQGVRN 300  
 DB 265 EAVGLPSIPVHPICGYDAKLEKNGSAPDSSNKGSLKVPYWGPGFQNPFSNQGVRN 344  
 QY 301 HINSTNEVTRIVYIGTLKCAVDPDRVYLGGHBSWFGIDPQSGAAVHETVSPGT 360  
 DB 345 HINSTNEVTRIVYIGTLKCAVDPDRVYLGGHBSWFGIDPQSGAAVHETVSPGT 404  
 QY 361 LKFGCHRRPRTILPASHDAEFVGLGSTDAENRSLQERGVATINDGSIKONTYLV 420  
 DB 405 LKFGCHRRPRTILPASHDAEFVGLGSTDAENRSLQERGVATINDGSIKONTYLV 464  
 QY 421 DCPYLVATLNLKTELSKSPDPCFSGSLSEKFTKSPGPPGQMRISLIGSNDPFGY 480  
 DB 465 DCPYLVATLNLKTELSKSPDPCFSGSLSEKFTKSPGPPGQMRISLIGSNDPFGY 524  
 QY 481 RORLCILSGNAVYVWVWVNSGCPRLVSVYVETVYKFDPMKXVYVYVQVPGGV 540  
 DB 525 RORLCILSGNAVYVWVWVNSGCPRLVSVYVETVYKFDPMKXVYVYVQVPGGV 584  
 QY 541 PEANSLVLPFCRDVYVYVLRNKAADITSISNKHQDPTVCGSPDSISNKNKPEAS 600  
 DB 585 PEANSLVLPFCRDVYVYVLRNKAADITSISNKHQDPTVCGSPDSISNKNKPEAS 644  
 QY 601 KFSBRLODPKSNRIVLBNKQDLKPLRN 628  
 DB 645 KFSBRLODPKSNRIVLBNKQDLKPLRN 673

RESOLV 17  
ID Y92632 standard: Protein: 750 AA.  
AC Y92632:  
DB 10-AUG-2000 (first entry)  
XX Mutant human prostate specific membrane antigen construct, hPSM1.8.  
XX Prostate specific membrane antigen; immunogenized construct; mutant;  
XX vasculature; cytotoxic T-lymphocyte immunity; breast cancer;  
XX prostate cancer; cell-associated peptide antigen; foreign epitope.  
XX Homo sapiens.  
XX Synthetic.  
XX Key Location/Qualifiers  
XX Peptide 24..38  
XX /label= P2  
XX /note= "foreign epitope"  
XX /note= "foreign epitope"  
XX /note= "foreign epitope"  
XX MO20020027-A2.  
XX 13-APR-2000.  
XX 05-OCT-1999: 99M0-DR00525.  
XX 05-OCT-1998: 98M0-0001261.  
XX 20-OCT-1998: 98M0-0105011.  
XX (MEDI-) M & E BIOTECH AS.  
XX Steina L. Moutsean S. Nilsen KC. Henning J. Leach D. Dajum I.  
XX Gautam A. Birk P. Karlsson G.  
XX WPI: 2000-349917/30.  
XX Inducing immune responses to weakly immunogenic, tumor associated  
XX peptide antigens for the treatment of breast and prostate cancer  
XX Example 1: Page -: 220pp; English.  
XX Y92632-49 are mutant immunogenized human prostate specific membrane  
XX antigen (PSM) constructs, which contain foreign epitopes (P2 and/or P30).  
XX The immunogenic analogues of PSM can be used in the claimed method as an

CC autoantigen to induce a CTL response. Subdominant CTL epitopes, antibody  
CC binding regions and cysteine residues involved in disulfide bonds are  
CC preserved in the immunogenized forms. The method is used for inducing  
CC immune responses against weakly immunogenic, tumor associated  
CC antigens (PA) such as those associated with cancers (cell proteins), e.g.,  
CC human prostate specific membrane antigen (PSM), heparin 2 (he2) and/or  
CC fibroblast growth factor 8b (FGF8b). The method comprises effecting  
CC immunogen presentation by antigen producing cells (APCs) of the  
CC animal immune system (e.g., human) to the CTLs (e.g., human CTLs).  
CC group derived from the PA and/or at least 1 B-cell group derived from the  
CC cell-associated PA; and (2) at least 1 first T helper cell group which is  
CC foreign to the animal. Analogues of human PSM, human he2 and  
CC human FGF8b are immunogenized in the form of a construct, including at  
CC least one foreign T helper epitope of the respective PA and including at  
CC least one foreign T helper epitope of the respective PA and including at  
CC Note: This sequence was constructed from the wild type human PSM  
CC (Y92619), which appears on pages 184-187 of the specification.  
XX Sequence 750 AA:  
SQ  
Query Match 79.6%; Score 561; DB 21; Length 750;  
Best Local Similarity 100.0%; Pred No. 0;  
Matches 561; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SSNENATPNNHKAFLDELANIKKFLNFQPHLAGTQNMOLANQISQMGKRC 60  
DB 45 aaeatnlrphhmkatldelkaenlkfytqphlagteqnlakqyqvekf 104  
QY 61 LDSELANIDVLLSPNKTGPNYISIIINQGNKFTFSLPEPPGCEYNDVTPPSAF 120  
DB 105 ldsvelahydllypnkthpyislindgncfhtalcfepppyevndlvptsaef 164  
QY 121 SPQAPGQDLYVNNATPEPPKFLPEPNTSGRTYIAGKRCYVNNALQANG 180  
DB 165 eppgmpesqlvyymyatfedfletcdnkncskvltarykyvfnhnaqaaag 224  
QY 181 VTXSDNATVNNACSTFPOCKNLPGCGVQCNILNKACDPLPQTPANETATKCA 240  
DB 225 vlyedpadyfepkyepedpnlppgyvgnlnlnsgdpltpypaneyvyrtsla 284  
QY 241 RAVGLPSIVPPTGVDAKILKMKCGAPSSWNGSLKLVYVNGPSPGSPQVYPM 300  
DB 285 eevglpdlpnylyydaqlklemgagadpnygllypyvpylqngncknck 344  
QY 301 HTHTNPTRTYVLTGLKAVPDRVYLGSHDSBWPQGDIDGSAVNHVTSAPGT 360  
DB 345 hthntvrtvlyvgtlsgvdpdpylsgnldewvsgldqpsavnhvltvsgc 404

QY 361 LKKEQPPERTILFASWAEPPQLCSFPAENRSLGRCYVNNAGTQNTLAV 420  
DB 405 lkkeqppertllfawdeefglstevaeenarllqeyvaylnadaaleqnytliv 464  
QY 421 DCEPLATSYVNNLNEIASPDRTKSLTSPKSPSPFGQPNISKLSCGNDPEP 480  
DB 465 dceplmalyvnhltelkspdeglkelyeevltkppetlqprltklsgndleiv 524  
QY 481 PQLGASGRATTTNMTKNSCYPLVHSVETTELKPEPDNFKHLMVAQNRGCV 540  
DB 528 qplglsaggrattnmtknsqplvhsvettelkpepdnfrkhlmtvaqrgcv 584  
QY 541 PELANSIVPDCRDYAVVYLRK 562  
DB 585 pelansivpdcrdcyavvylrk 606  
RESOLV 18  
ID Y92629 standard: Protein: 750 AA.  
AC Y92629:  
DB 10-AUG-2000 (first entry)  
XX Mutant human prostate specific membrane antigen construct, hPSM8.1.  
XX Prostate specific membrane antigen; immunogenized construct; mutant;  
XX vasculature; cytotoxic T-lymphocyte immunity; breast cancer;  
XX prostate cancer; cell-associated peptide antigen; foreign epitope.  
XX Homo sapiens.  
XX Synthetic.  
XX Key Location/Qualifiers  
XX Peptide 21..41  
XX /label= P30  
XX /note= "foreign epitope"  
XX /label= P2  
XX /note= "foreign epitope"  
XX MO20020027-A2.  
XX 13-APR-2000.  
XX 05-OCT-1999: 99M0-DR00525.  
XX 05-OCT-1998: 98M0-0001261.  
XX 20-OCT-1998: 98M0-0105011.  
XX

PA (MEDI-) M & E BIOTECH AS.  
XX Steina L. Moutsean S. Nilsen KC. Henning J. Leach D. Dajum I.  
XX Gautam A. Birk P. Karlsson G.  
XX WPI: 2000-349917/30.  
XX Inducing immune responses to weakly immunogenic, tumor associated  
XX peptide antigens for the treatment of breast and prostate cancer  
XX Example 1: Page -: 220pp; English.  
XX Y92632-49 are mutant immunogenized human prostate specific membrane  
XX antigen (PSM) constructs, which contain foreign epitopes (P2 and/or P30).  
XX The immunogenic analogues of PSM can be used in the claimed method as an  
XX autoantigen to induce a CTL response. Subdominant CTL epitopes, antibody  
XX binding regions and cysteine residues involved in disulfide bonds are  
XX preserved in the immunogenized forms. The method is used for inducing  
XX immune responses against weakly immunogenic, tumor associated  
XX antigens (PA) such as those associated with cancers (self-proteins), e.g.,  
XX human prostate specific membrane antigen (PSM), heparin 2 (he2), and/or  
XX fibroblast growth factor 8b (FGF8b). The method comprises effecting  
XX immunogen presentation by antigen producing cells (APCs) of the  
XX animal immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte)  
XX group derived from the PA and/or at least 1 B-cell group derived from the  
XX cell-associated PA; and (2) at least 1 first T helper cell group which is  
XX foreign to the animal. Analogues of human PSM, human he2 and  
XX human FGF8b are immunogenized in the form of a construct, including at  
XX least one foreign T helper epitope of the respective PA and including at  
XX Note: This sequence was constructed from the wild type human PSM  
XX (Y92619), which appears on pages 184-187 of the specification.  
XX Sequence 750 AA:  
SQ  
Query Match 79.5%; Score 561; DB 21; Length 750;  
Best Local Similarity 100.0%; Pred No. 0;  
Matches 561; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SSNENATPNNHKAFLDELANIKKFLNFQPHLAGTQNMOLANQISQMGKRC 60  
DB 45 aaeatnlrphhmkatldelkaenlkfytqphlagteqnlakqyqvekf 104  
QY 61 LDSELANIDVLLSPNKTGPNYISIIINQGNKFTFSLPEPPGCEYNDVTPPSAF 120  
DB 105 ldsvelahydllypnkthpyislindgncfhtalcfepppyevndlvptsaef 164  
QY 121 SPQAPGQDLYVNNATPEPPKFLPEPNTSGRTYIAGKRCYVNNALQANG 180





P1 Steina L, Mourleem S, Nielsen KG, Heaning J, Leach D, Dalum I:  
 P2 Gautier A, Birk P, Rafelsen G:  
 DB WPI: 2000-345917/30.  
 CC Inducing immune responses to weakly immunogenic, tumor associated  
 CC peptide antigens for the treatment of breast and prostate cancer  
 CC  
 CC Example 1: Page 1, 220pp, English.  
 CC  
 CC Y9267-49 are mutant immunogenic human prostate specific membrane  
 CC antigen (PSM) constructs, which contain foreign epitopes (P2 and/or P30).  
 CC The immunogenicity of PSMs is evaluated by immunizing mice with  
 CC adjuvant to induce a CTL response. Subdominant CTL epitopes, antibody  
 CC binding regions and cysteine residues involved in disulfide bonds are  
 CC preserved in the immunogenized forms. The method is used for inducing  
 CC immune responses against weakly immunogenic cell-associated peptide  
 CC antigens (PA) such as those associated with cancer (self-proteins), e.g.  
 CC human prostate specific membrane antigen (PSM), heregulin 2 (Hr2) and/or  
 CC fibroblast growth factor Bb (FGFB). The method comprises effecting  
 CC simultaneous presentation by antigen producing cells (APCs) of the  
 CC antigen (PA) and at least one foreign T helper cell group derived from the  
 CC cell-associated PA; and (2) at least a first T helper cell group which is  
 CC foreign to the animal. Analogues of human PSM, human Hr2 and  
 CC human/murine FGFB comprising a substantial part of all known and  
 CC predicted CTL and B-cell epitopes are also claimed. The method is used  
 CC to treat prostate, prostate/breast or breast cancer when the PA is human  
 CC PSM, FGFB and Hr2, respectively.  
 CC Note: This sequence was constructed from the valid type human PSM  
 CC (Y92615), which appears on pages 184-187 of the specification.  
 CC  
 CC Sequence 693 AA:  
 50

Query Match 62.7% Score 443 DB 21 Length 693:  
 Best Local Similarity 100.0% Pred. No. 0:  
 Matches 443: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 187 PVDYFACVYKSTYPCDNLKSGCVRGICLAKGACDPTGCPYANFVYRNIADLACVLP 246  
 DB 174 PVDYFACVYKSTYPCDNLKSGCVRGICLAKGACDPTGCPYANFVYRNIADLACVLP 233  
 QY 247 STVHPDGTDAKLEKMGDAPDSSWNGSLKVPYVWGPFCFNGFSTOKYKMHINSTN 306  
 DB 234 STVHPDGTDAKLEKMGDAPDSSWNGSLKVPYVWGPFCFNGFSTOKYKMHINSTN 293  
 QY 307 EVTRIVYVIGTILGAVEDRYVIGLGRHDSVPGCIDPGSGAAVHIEVSGFTLEKEDW 366  
 DB 294 EVTRIVYVIGTILGAVEDRYVIGLGRHDSVPGCIDPGSGAAVHIEVSGFTLEKEDW 353

QY 367 RPRRTILFASNDAREPGLSTERNABENSHLLAQRCVNIYINADSSITSCNTYTLNDCCPIM 426  
 DB 354 RPRRTILFASNDAREPGLSTERNABENSHLLAQRCVNIYINADSSITSCNTYTLNDCCPIM 413  
 QY 427 YSLVYHNTRELKSPDGFSEKSLYSEWTKSPSPFSSQSRISRLSGDQVEYFPOULI 486  
 DB 414 YSLVYHNTRELKSPDGFSEKSLYSEWTKSPSPFSSQSRISRLSGDQVEYFPOULI 473  
 QY 487 ASGARVYKMEZNFSGVPLHSHVETVELVEFYDPEKIKHLTVAGVRCGVAFELANS 546  
 DB 474 ASGARVYKMEZNFSGVPLHSHVETVELVEFYDPEKIKHLTVAGVRCGVAFELANS 533  
 QY 547 YVDPDNDYAVVLAERKADKITSISNKPDEKITSVSPDSIPSAVKNFTSLSPFEEL 606  
 DB 534 YVDPDNDYAVVLAERKADKITSISNKPDEKITSVSPDSIPSAVKNFTSLSPFEEL 593  
 QY 607 GQPDKSNPVTYRMDNDLMEFLER 629  
 DB 594 GQPDKSNPVTYRMDNDLMEFLER 616  
 RESULT 23  
 Y92646  
 ID Y92646 standard: Protein: 750 AA.  
 XX Y92646:  
 DT 10-ANC-2000 (first entry)  
 CC  
 CC Mutant human prostate specific membrane antigen construct, hPSM10.3.  
 CC Prostate specific membrane antigen: immunogenized construct; mutant:  
 CC vaccination: cytotoxic T-lymphocyte immunity; breast cancer:  
 CC prostate cancer: cell-associated peptide antigen; foreign epitope:  
 CC  
 CC Homo sapiens.  
 CC Synthetic.  
 CC  
 CC Key Location/Qualifiers  
 CC P2 /label= P2  
 CC Peptide /note= "foreign epitope"  
 CC 210..230  
 CC /label= P30  
 CC /note= "foreign epitope"  
 CC  
 CC W0200020027-A2.  
 CC  
 CC 13-APR-2000.

P1 Steina L, Mourleem S, Nielsen KG, Heaning J, Leach D, Dalum I:  
 P2 Gautier A, Birk P, Rafelsen G:  
 DB WPI: 2000-345917/30.  
 CC Inducing immune responses to weakly immunogenic, tumor associated  
 CC peptide antigens for the treatment of breast and prostate cancer  
 CC  
 CC Example 1: Page 1, 220pp, English.  
 CC  
 CC Y9267-49 are mutant immunogenic human prostate specific membrane  
 CC antigen (PSM) constructs, which contain foreign epitopes (P2 and/or P30).  
 CC The immunogenicity of PSMs is evaluated by immunizing mice with  
 CC adjuvant to induce a CTL response. Subdominant CTL epitopes, antibody  
 CC binding regions and cysteine residues involved in disulfide bonds are  
 CC preserved in the immunogenized forms. The method is used for inducing  
 CC immune responses against weakly immunogenic cell-associated peptide  
 CC antigens (PA) such as those associated with cancer (self-proteins), e.g.  
 CC human prostate specific membrane antigen (PSM), heregulin 2 (Hr2) and/or  
 CC fibroblast growth factor Bb (FGFB). The method comprises effecting  
 CC simultaneous presentation by antigen producing cells (APCs) of the  
 CC antigen (PA) and at least one foreign T helper cell group derived from the  
 CC cell-associated PA; and (2) at least a first T helper cell group which is  
 CC foreign to the animal. Analogues of human PSM, human Hr2 and  
 CC human/murine FGFB comprising a substantial part of all known and  
 CC predicted CTL and B-cell epitopes are also claimed. The method is used  
 CC to treat prostate, prostate/breast or breast cancer when the PA is human  
 CC PSM, FGFB and Hr2, respectively.  
 CC Note: This sequence was constructed from the valid type human PSM  
 CC (Y92615), which appears on pages 184-187 of the specification.  
 CC  
 CC Sequence 750 AA:  
 50

QY 247 STVHPDGTDAKLEKMGDAPDSSWNGSLKVPYVWGPFCFNGFSTOKYKMHINSTN 306  
 DB 201 STVHPDGTDAKLEKMGDAPDSSWNGSLKVPYVWGPFCFNGFSTOKYKMHINSTN 350  
 QY 307 EVTRIVYVIGTILGAVEDRYVIGLGRHDSVPGCIDPGSGAAVHIEVSGFTLEKEDW 366  
 DB 351 EVTRIVYVIGTILGAVEDRYVIGLGRHDSVPGCIDPGSGAAVHIEVSGFTLEKEDW 410  
 QY 367 RPRRTILFASNDAREPGLSTERNABENSHLLAQRCVNIYINADSSITSCNTYTLNDCCPIM 426  
 DB 411 RPRRTILFASNDAREPGLSTERNABENSHLLAQRCVNIYINADSSITSCNTYTLNDCCPIM 470  
 QY 427 YSLVYHNTRELKSPDGFSEKSLYSEWTKSPSPFSSQSRISRLSGDQVEYFPOULI 486  
 DB 471 YSLVYHNTRELKSPDGFSEKSLYSEWTKSPSPFSSQSRISRLSGDQVEYFPOULI 530  
 QY 487 ASGARVYKMEZNFSGVPLHSHVETVELVEFYDPEKIKHLTVAGVRCGVAFELANS 546  
 DB 531 ASGARVYKMEZNFSGVPLHSHVETVELVEFYDPEKIKHLTVAGVRCGVAFELANS 590  
 QY 547 YVDPDNDYAVVLAERKADKITSISNKPDEKITSVSPDSIPSAVKNFTSLSPFEEL 606  
 DB 591 YVDPDNDYAVVLAERKADKITSISNKPDEKITSVSPDSIPSAVKNFTSLSPFEEL 650  
 QY 607 GQPDKSNPVTYRMDNDLMEFLER 629  
 DB 651 GQPDKSNPVTYRMDNDLMEFLER 673  
 RESULT 24  
 Y92639  
 ID Y92639 standard: Protein: 750 AA.  
 XX Y92639:  
 DT 10-ANC-2000 (first entry)  
 CC  
 CC Mutant human prostate specific membrane antigen construct, hPSM5.1.  
 CC Prostate specific membrane antigen: immunogenized construct; mutant:  
 CC vaccination: cytotoxic T-lymphocyte immunity; breast cancer:  
 CC prostate cancer: cell-associated peptide antigen; foreign epitope:  
 CC  
 CC Homo sapiens.  
 CC Synthetic.  
 CC  
 CC Key Location/Qualifiers  
 CC P2 /label= P2  
 CC Peptide /note= "foreign epitope"  
 CC 21..41  
 CC /label= P30  
 CC /note= "foreign epitope"  
 CC  
 CC Peptide 305..319

[illegible]

Query Match 61.0%; Score 431; DB 21; Length 750

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Mon Apr 9 11:14:10 2001
us-003-803-72.cop3.45.750.o11g.xag

OS      Synthetic.
FH      Key
FH      Peptide
FH      /Label_P2
FH      /Label_1930
FH      /Label_P30
FH      /note "foreign epitope"
FH      Peptide
FH      /note "foreign epitope"
PN      M0200020027-A2.
PD      13-APR-2000.
PE      05-OCT-1999; 99MO-DX00525.
PR      05-OCT-1998; 98BK-0001261.
PR      20-OCT-1998; 9803-015011.
PA      (MEDI) M & E BIOCHEM AS
P1      Stelina L, Mourliens S, Nielsen KG, Heaning J, Leach D, Daltum I;
P2      Gudatun M, Birk P, Matheson G.
P3      WPI; 2000-134991/30.
PX      Inducing immune response to locally immunogenic, tumor associated
PX      peptide antigens for the treatment of breast and prostate cancer
PX
PS      Example 1; Page 1; 220pp; English.
CC      Y32637-49 are mutant immunogenized human prostate specific membrane
CC      antigen (PSM) constructs, which contain foreign epitopes (P2 and/or P3)
CC      The immunogenicity of PSM can be used in the claimed method as a
CC      bioindicator to induce a CTL response. Subdominant CTL epitopes, antibody
CC      binding site, and the immunogenicity of PSM can be used in the claimed
CC      method as a bioindicator to induce a CTL response. The method is used for inducing
CC      immune responses against weakly immunogenic cell-associated peptide
CC      antigens (PA) such as those associated with cancers (self-proteins), e.g.
CC      ribonucleic growth factor (bFGF), the epidermal growth factor (EGF),
CC      simian virus 40 (SV40) large T antigen (TAg), and the human papilloma virus
CC      (HPV) E6 and E7 proteins. The method is used for inducing immune responses
CC      against immune system of (1) at least 1 CTL (cytotoxic T-lymphocyte)
CC      cell-associated PA, and (2) at least 1 B-cell group derived from
CC      cells associated PA, and (3) at least 1 T-cell group derived from
CC      foreign to the animal. Antigens of human PSM, human Her2 and
CC      human-oncogene PSM comprising a substantial part of all known and
CC      least one foreign T cell epitopes of the respective PA, and including
CC      at least one foreign T cell epitope of the respective PA, and including
CC      to treat prostate, prostate/breast or breast cancer when the PA is human
CC      PSM, PGPBst and Her2, respectively.

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[illegible]

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Page 80

[illegible]



CC cell-associated PA, and (2) at least 1 first T helper cell group which is foreign to the animal. Analogues of human PSM, human HcY and PSM humanized, and PSM comprising a species of the respective PA and at least one foreign T helper epitope are also claimed. The method is used to treat prostate, reproductive/ breast or breast cancer when the PA is human PSM, PSM, HcY and HcY, respectively.

CC The invention also relates to a method of identifying a first type human PSM (192619), which appears on pages 184-187 of the specification.

XX

SQ Sequence 750 AA:

Seq Match 57.1% Score 403: DB 21: Length 750: Query  
Beat Local Similarity 100.0% Pred. No. 0: Gaps 0  
Matches 403: Conservative 0: Mismatches 0: Indels 0: Open

0Y 1 GSNKADPDAITKNNKAFLEKLEKREKFLNPNQIPLAGTQEPNOLQKIOSQEMFC 60  
45 senechvfkhnkksfidekneklkltymtqtblvqemqlkdkqkqveieg 104  
0Y 1 LSGEELATVYGLLEVPYNNKHITISINQKQKSPFTSELEPPKPCQKENVDPVPSNF 120  
60 lsdgelaivnytllygkchbnyflinldngneflaklepppnyamdyvprapl 164  
0Y 1 SPQKPEPDADYVAVAFKPEPFRPHNINISCTATVAKYKQKGVNVMQKQAKG 180  
60 spqkpepdadyvavafedrfllnkmlncskglavlaeyrfygnvbnqalagab 224  
0Y 1 VTSRPPADYAPKQVQSTPSPHNNKQKQKCHIKNNKQKPTQVPAWYKAPGKIA 240  
60 vtsrppadyapkvqvstpsphnnkqkqkchiknnkqkptqvpaawykyapgkia 284  
0Y 225 vlyqpdagdyfepvnyvayvaflllbgggvqyaflllbgagpdlfrygnyvaytga 300  
60 vlyqpdagdyfepvnyvayvaflllbgggvqyaflllbgagpdlfrygnyvaytga 344  
0Y 285 eavqjzspvphjyvdagqlflbmaggspdpasavqsllyvqnyvqfsgnlsqkvlm 360  
60 eavqjzspvphjyvdagqlflbmaggspdpasavqsllyvqnyvqfsgnlsqkvlm 404  
0Y 301 hlsatetvnyvaytgcflacavpnyvylcglsbqkqkqkcdpocakllyvnyvsgt 350  
60 hlsatetvnyvaytgcflacavpnyvylcglsbqkqkqkcdpocakllyvnyvsgt 404  
0Y 345 hlsatetvnyvaytgcflacavpnyvylcglsbqkqkqkcdpocakllyvnyvsgt 404  
60 hlsatetvnyvaytgcflacavpnyvylcglsbqkqkqkcdpocakllyvnyvsgt 447

DB 361 LKSGKQKRRRLTFLASNDKAEKPLQSTGMAEENSLKSLQKQV 403  
405 lksgkqkrrrltflasndkAEKPLQSTGMAEENSLKSLQKQV 403

SEQUENCE 27  
ID Y92631  
AC Y92631 standard: Protein: 750 AA.  
NC Y92631:

[illegible]



```

CC antigen (PSM) constructs, which contain foreign epitopes (p2 and/or p30).
CC The immunogenic analogues of PSM can be used in the claimed method as a
CC binding regions and cysteine residues involved in disulfide bonds are
CC preserved in the immunogenized forms. The method is used for inducing
CC immune responses against weakly immunogenic cell-associated peptide
CC antigens (PA), such as the tumor-associated antigen (PSM) resulting in p2 and/or
CC fibroblast growth factor (bFGFb). The method comprises effecting
CC simultaneous presentation by antigen producing cells (APCs) of the
CC cellular immune system of: (1) at least 1 CTL (cytotoxic T lymphocyte)
CC cell-associated PA, and (2) at least 1 TcT (helper cell) group which is
CC foreign to the animal. Analogues of human PSM, human HcT2 and
CC human/murine FcGfB comprising a substantial part of all known and
CC predicted CTL and TcT epitopes of PSM are claimed. The method is used
CC to treat prostate, prostate/breast or breast cancer when the PA, as
CC PSM, FcGfB and HcT2, respectively.
CC Note: This sequence was constructed from the wild type human PSM
CC (p35p39), which appears on pages 104-107 of the specification.
CC
CC
CC Sequence 693 AA:
CC
CC
CC Query Match 40.98; score 289; DB 21; Length 693;
CC Read Local Similarity 100.0%; Pred. No. 9-5e-281;
CC Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0
CC
CC 418 LKNCQPMYAWYVUNMNTLSPGDSQDPRKATYSKSTSTSPSPSSQSGHSTSLGSDMDY 477
CC Db 405 LKEDCPMLSTVYMLHLLTSPGDSQDPRKATYSKSTSTSPSPSSQSGHSTSLGSDMDY 464
CC 418 ENYDQDQASGATATFMMNMGSCGATKASVSTSTSPSPSSQSGHSTSLGSDMDY 537
CC Db 465 ENYDQDQASGATATFMMNMGSCGATKASVSTSTSPSPSSQSGHSTSLGSDMDY 524
CC 418 EVTFGLSTASSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTST 524
CC Db 418 EVTFGLSTASSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTST 524
CC 538 GWTEPLANSVLSPGCDGAVLVLRADLSTISLHNRDQKRTTIVSDSLSAKNTKE 597
CC Db 525 GWTEPLANSVLSPGCDGAVLVLRADLSTISLHNRDQKRTTIVSDSLSAKNTKE 584
CC 596 IAKRSTSLDQDSDSPVLTANNQDQKLTSLRATDTPGAGPPTPTPTPTPTPTPTPTPTPT 657
CC Db 585 IAKRSTSLDQDSDSPVLTANNQDQKLTSLRATDTPGAGPPTPTPTPTPTPTPTPTPTPT 644
CC 656 GSGSPSTGLDPLSDGSPVLEKSNQKQKQVLAFLPQAAKSTSLVA 706
CC Db 645 GSGSPSTGLDPLSDGSPVLEKSNQKQKQVLAFLPQAAKSTSLVA 693

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[illegible]

10-AUG-2000 (first entry)  
Murine prostate specific membrane antigen splice variant.  
Prostate specific membrane antigen, splice variant; vaccination;  
murine prostate specific membrane antigen, splice variant; cancer; breast cancer;  
prostate cancer; cell-associated peptide antigen; foreign epitope.  
Mus musculus.  
M0200020027-A2.  
13-APR-2000.  
05-OCT-1999: 99MO-DK00525.  
05-OCT-1998: 98DK-0001261.  
20-OCT-1998: 98DS-0105011.  
(M021-) M & E BIOTECH AS.  
Steinaa L, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;  
Gautam A, Birik P, Karlsson G;  
WPI: 2000-349917/30.  
N-PSDB: A09459.  
Inducing immune responses to weakly immunogenic, tumor associated  
peptide antigens for the treatment of breast and prostate cancer  
Example 1: Page 210-213: 220pp: English.  
The claims detail a method for inducing immune responses against weakly  
immunogenic cell-associated peptide antigens (PA), for example, human  
prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or  
fibroblast growth factor 8b (FGF8b). The method comprises effecting  
the immunization of an animal by antigen producing cells (APCs) of the  
animal immune system (e.g., murine splenic dendritic cells) with a  
cell-associated PA; and (2) at least a first T helper cell group derived from the  
animal, analogues of human PSM, human Her2 and human FGF8b, and  
foreign to the animal. Analogues of human PSM, human Her2 and  
human FGF8b, and foreign to the animal, are also claimed. The method is used  
to treat prostate, prostate/breast or breast cancer when the PA is human  
PSM, FGF8b and Her2, respectively.  
Sequence 694 AA:

Y92659-62 are mutant immunogenized murine prostate specific membrane  
antigen (PSM) constructs, which contain a foreign epitope, p30.  
Analogues can be used to study whether auto-tolerance to mouse PSM can be  
broken in mice by immunisation and/or DNA vaccination against murine PSM  
using murine PSM analogues. Immunogenic analogues of PSM can be used in  
method is used for inducing immune responses against weakly immunogenic  
cell-associated peptide antigens (PA) such as those associated with  
cancers (e.g., human PSM, heregulin 2 (Her2) and/or  
fibroblast growth factor 8b (FGF8b)). The method comprises effecting  
the immunization of an animal by antigen producing cells (APCs) of the  
animal immune system (e.g., murine splenic dendritic cells) with a  
cell-associated PA; and (2) at least a first T helper cell group derived from the  
animal, analogues of human PSM, human Her2 and human FGF8b, and  
foreign to the animal. Analogues of human PSM, human Her2 and  
human FGF8b, and foreign to the animal, are also claimed. The method is used  
to treat prostate, prostate/breast or breast cancer when the PA is human  
PSM, FGF8b and Her2, respectively.  
Note: This sequence was constructed from the murine PSM splice variant  
(Y92654), which appears on pages 210-213 of the specification.  
Sequence 698 AA:  
Query Match 5.1%; Score 36; DB 21; Length 698;  
Best Local Similarity 100.0%; Pred. No. 14e-28;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
395 SRLLGRCVATINDSIEGNTLRVDCPTPLRYSLV 430  
DB 387 srllgrcvayindaslegnytlrvdcptplryslv 422  
RESULT 34  
Y92662  
13-APR-2000.  
192662 standard: Protein: 703 AA.  
AC Y92662:  
10-AUG-2000 (first entry)  
Mutant murine PSM splice variant construct, mPSM.Y.  
Prostate specific membrane antigen, splice variant; mutant;  
vaccination; cytotoxic T-lymphocyte immunity; breast cancer;  
prostate cancer; cell-associated peptide antigen; foreign epitope.  
Mus musculus.  
Synthetic.  
Sequence 703 AA:

Query Match 5.1%; Score 36; DB 21; Length 694;  
Best Local Similarity 100.0%; Pred. No. 14e-28;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
395 SRLLGRCVATINDSIEGNTLRVDCPTPLRYSLV 430  
DB 387 srllgrcvayindaslegnytlrvdcptplryslv 418  
RESULT 33  
Y92661  
13-APR-2000.  
192661 standard: Protein: 698 AA.  
AC Y92661:  
10-AUG-2000 (first entry)  
Mutant murine PSM splice variant construct, mPSM.X.  
Prostate specific membrane antigen, splice variant; mutant;  
vaccination; cytotoxic T-lymphocyte immunity; breast cancer;  
prostate cancer; cell-associated peptide antigen; foreign epitope.  
Mus musculus.  
Synthetic.  
Sequence 703 AA:  
Query Match 5.1%; Score 36; DB 21; Length 694;  
Best Local Similarity 100.0%; Pred. No. 14e-28;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
395 SRLLGRCVATINDSIEGNTLRVDCPTPLRYSLV 430  
DB 387 srllgrcvayindaslegnytlrvdcptplryslv 418  
RESULT 33  
Y92661  
13-APR-2000.  
192661 standard: Protein: 698 AA.  
AC Y92661:  
10-AUG-2000 (first entry)  
Mutant murine PSM splice variant construct, mPSM.X.  
Prostate specific membrane antigen, splice variant; mutant;  
vaccination; cytotoxic T-lymphocyte immunity; breast cancer;  
prostate cancer; cell-associated peptide antigen; foreign epitope.  
Mus musculus.  
Synthetic.  
Sequence 703 AA:  
Query Match 5.1%; Score 36; DB 21; Length 694;  
Best Local Similarity 100.0%; Pred. No. 14e-28;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
395 SRLLGRCVATINDSIEGNTLRVDCPTPLRYSLV 430  
DB 387 srllgrcvayindaslegnytlrvdcptplryslv 418  
RESULT 33  
Y92661  
13-APR-2000.  
192661 standard: Protein: 698 AA.  
AC Y92661:  
10-AUG-2000 (first entry)  
Mutant murine PSM splice variant construct, mPSM.X.  
Prostate specific membrane antigen, splice variant; mutant;  
vaccination; cytotoxic T-lymphocyte immunity; breast cancer;  
prostate cancer; cell-associated peptide antigen; foreign epitope.  
Mus musculus.  
Synthetic.  
Sequence 703 AA:

Y92659-62 are mutant immunogenized murine prostate specific membrane  
antigen (PSM) constructs, which contain a foreign epitope, p30.  
Analogues can be used to study whether auto-tolerance to mouse PSM can be  
broken in mice by immunisation and/or DNA vaccination against murine PSM  
using murine PSM analogues. Immunogenic analogues of PSM can be used in  
method is used for inducing immune responses against weakly immunogenic  
cell-associated peptide antigens (PA) such as those associated with  
cancers (e.g., human PSM, heregulin 2 (Her2) and/or  
fibroblast growth factor 8b (FGF8b)). The method comprises effecting  
the immunization of an animal by antigen producing cells (APCs) of the  
animal immune system (e.g., murine splenic dendritic cells) with a  
cell-associated PA; and (2) at least a first T helper cell group derived from the  
animal, analogues of human PSM, human Her2 and human FGF8b, and  
foreign to the animal. Analogues of human PSM, human Her2 and  
human FGF8b, and foreign to the animal, are also claimed. The method is used  
to treat prostate, prostate/breast or breast cancer when the PA is human  
PSM, FGF8b and Her2, respectively.  
Note: This sequence was constructed from the murine PSM splice variant  
(Y92654), which appears on pages 210-213 of the specification.  
Sequence 703 AA:  
Query Match 5.1%; Score 36; DB 21; Length 698;  
Best Local Similarity 100.0%; Pred. No. 14e-28;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
395 SRLLGRCVATINDSIEGNTLRVDCPTPLRYSLV 430  
DB 387 srllgrcvayindaslegnytlrvdcptplryslv 422  
RESULT 34  
Y92662  
13-APR-2000.  
192662 standard: Protein: 703 AA.  
AC Y92662:  
10-AUG-2000 (first entry)  
Mutant murine PSM splice variant construct, mPSM.Y.  
Prostate specific membrane antigen, splice variant; mutant;  
vaccination; cytotoxic T-lymphocyte immunity; breast cancer;  
prostate cancer; cell-associated peptide antigen; foreign epitope.  
Mus musculus.  
Synthetic.  
Sequence 703 AA:

Query Match 5.1% Score 36 DB 21 Length 703  
Best Local Similarity 100.0% Pred. No. 1.5e-28  
Matches 36: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 395 SLLAGRGVATINADSGIRGWTATNOCPTATSLV 430  
DB 383 SLTIGGVAYINADSLSPYLTVCPPIAYALV 418

RESULT 35  
Y92659 standard: Protein: 752 AA.

AC Y92659:  
10-NOV-2000 (first entry)  
Murine prostate specific membrane antigen.  
Prostate specific membrane antigen, aplice variant, vaccination;  
cytotoxic T-lymphocyte immunity; self-protein superantigen;  
prostate cancer; cell-associated peptide antigen; foreign epitope.  
Mus maculuss.  
MO200020027-A2.  
13-APR-2000.  
05-OCT-1999: 99MO-DK00525.  
05-OCT-1998: 98DK-0001261.  
20-OCT-1998: 98OS-0105011.  
(M8B1-) M & E BIOTECH AS.  
Stelma L, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;  
Gautam A, Birk P, Karlsson G;  
WPI: 2000-349317/30.  
N-PSDB: A09458.  
Inducing immune responses to weakly immunogenic, tumor associated  
peptide antigens for the treatment of breast and prostate cancer  
Example 1: Page 204-206; 220pp: English.

The claim detail a method for inducing immune responses against weakly  
immunogenic peptide antigens for the treatment of breast and prostate cancer  
associated with cancers (i.e. self-proteins), for example human

XX 05-OCT-1998: 98DK-0001261.  
PR 20-OCT-1998: 98OS-0105011.  
PA (M8B1-) M & E BIOTECH AS.  
XX Stelma L, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;  
PI Gautam A, Birk P, Karlsson G;  
WPI: 2000-349317/30.  
Inducing immune responses to weakly immunogenic, tumor associated  
peptide antigens for the treatment of breast and prostate cancer  
Example 1: Page 204-206; 220pp: English.

XX Y92659-62 are mutant immunogenized murine prostate specific membrane  
antigen (PSM) constructs, which contain a foreign epitope, p30. The  
antigens can be used to study whether autotoxication against murine PSM  
can be broken in mice by immunisation and/or DNA vaccination against murine PSM  
using murine PSM analogues. Immunogenic analogues of PSM can be used in  
the claimed method as an autovaccine to induce a CTL response. The  
analogues are immunogenic analogues of the murine PSM, which is an  
cell-associated peptide antigen (PA) such as those associated with  
cancers (self-proteins), e.g. human PSM, heregulin 2 (Hr2) and/or  
fibroblast growth factor 8b (FGF8b). The method comprises effecting  
an animal immune system of: (1) at least one CTL (cytotoxic T-lymphocyte)  
group derived from the PA and/or at least 1 B-cell group derived from the  
cell-associated PA; and (2) at least 1 first T helper cell group which is  
foreign to the animal. Analogues of human PSM, human Hr2 and  
human FGF8b comprising a foreign epitope, p30, are also included.  
Predicted CTL and B-cell epitopes of the respective PA and including at  
least one foreign T helper epitope are also claimed. The method is used  
to treat prostate, prostate/breast or breast cancer when the PA is human  
PSM, Hr2 and Hr2, respectively.  
Note: This sequence was constructed from the wild type murine PSM  
(Y92623), which appears on pages 204-206 of the specification.

XX Sequence 756 AA:

Query Match 5.1% Score 36 DB 21 Length 756  
Best Local Similarity 100.0% Pred. No. 1.5e-28  
Matches 36: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 395 SLLAGRGVATINADSGIRGWTATNOCPTATSLV 430  
DB 445 SLTIGGVAYINADSLSPYLTVCPPIAYALV 480

CC prostate specific membrane antigen (PSM), heregulin 2 (Hr2) and/or  
CC fibroblast growth factor 8b (FGF8b), which are immunogenic  
CC analogues can be used to study whether autotoxication against murine PSM  
can be broken in mice by immunisation and/or DNA vaccination against murine PSM  
using murine PSM analogues. Immunogenic analogues of PSM can be used in  
the claimed method as an autovaccine to induce a CTL response. The  
analogues are immunogenic analogues of the murine PSM, which is an  
cell-associated PA; and (2) at least 1 first T helper cell group which is  
foreign to the animal. Analogues of human PSM, human Hr2 and  
human FGF8b comprising a foreign epitope, p30, are also included.  
Predicted CTL and B-cell epitopes of the respective PA and including at  
least one foreign T helper epitope are also claimed. The method is used  
to treat prostate, prostate/breast or breast cancer when the PA is human  
PSM, Hr2 and Hr2, respectively.

XX Sequence 752 AA:

Query Match 5.1% Score 36 DB 21 Length 752  
Best Local Similarity 100.0% Pred. No. 1.5e-28  
Matches 36: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 395 SLLAGRGVATINADSGIRGWTATNOCPTATSLV 430  
DB 441 SLTIGGVAYINADSLSPYLTVCPPIAYALV 476

RESULT 36  
Y92659 standard: Protein: 756 AA.

AC Y92659:  
10-NOV-2000 (first entry)  
Murine prostate specific membrane antigen construct, mPSM.  
Prostate specific membrane antigen; immunogenized construct; mutant;  
vaccination; cytotoxic T-lymphocyte immunity; breast cancer;  
prostate cancer; cell-associated peptide antigen; foreign epitope.  
Mus maculuss.  
MO200020027-A2.  
13-APR-2000.  
05-OCT-1999: 99MO-DK00525.

RESULT 37  
Y92660 standard: Protein: 761 AA.

AC Y92660:  
10-NOV-2000 (first entry)  
Murine prostate specific membrane antigen construct, mPSM.  
Prostate specific membrane antigen; immunogenized construct; mutant;  
vaccination; cytotoxic T-lymphocyte immunity; breast cancer;  
prostate cancer; cell-associated peptide antigen; foreign epitope.  
Mus maculuss.  
MO200020027-A2.  
13-APR-2000.  
05-OCT-1999: 99MO-DK00525.  
05-OCT-1998: 98DK-0001261.  
20-OCT-1998: 98OS-0105011.  
(M8B1-) M & E BIOTECH AS.  
Stelma L, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;  
PI Gautam A, Birk P, Karlsson G;  
WPI: 2000-349317/30.  
Inducing immune responses to weakly immunogenic, tumor associated  
peptide antigens for the treatment of breast and prostate cancer  
Example 1: Page 220pp: English.

XX Y92659-62 are mutant immunogenized murine prostate specific membrane  
antigen (PSM) constructs, which contain a foreign epitope, p30. The  
antigens can be used to study whether autotoxication against murine PSM  
can be broken in mice by immunisation and/or DNA vaccination against murine PSM  
using murine PSM analogues. Immunogenic analogues of PSM can be used in  
the claimed method as an autovaccine to induce a CTL response. The  
analogues are immunogenic analogues of the murine PSM, which is an  
cell-associated peptide antigen (PA) such as those associated with  
cancers (self-proteins), e.g. human PSM, heregulin 2 (Hr2) and/or  
fibroblast growth factor 8b (FGF8b). The method comprises effecting  
an animal immune system of: (1) at least one CTL (cytotoxic T-lymphocyte)  
group derived from the PA and/or at least 1 B-cell group derived from the  
cell-associated PA; and (2) at least 1 first T helper cell group which is  
foreign to the animal. Analogues of human PSM, human Hr2 and  
human FGF8b comprising a foreign epitope, p30, are also included.  
Predicted CTL and B-cell epitopes of the respective PA and including at  
least one foreign T helper epitope are also claimed. The method is used  
to treat prostate, prostate/breast or breast cancer when the PA is human  
PSM, Hr2 and Hr2, respectively.

XX Sequence 756 AA:



PA (SLOAN ) SLOAN KETTERING INST CANCER RES.  
 P1 PAIR NR, Heaton MDM, Israel RS.  
 XX WPI: 1996-402365/40.  
 DR DNA encoding alternatively applied prostate-specific membrane  
 XX antigen (PSM) development for detection of prostate cancer  
 XX micrometastatic tumour cells or prostate cancer progression  
 PT Example 1: Page 49: 284pp: English.  
 PS  
 CC Trypic peptides (M0237-45) were chid from the human prostate-  
 CC specific membrane (PSM) antigen (see also M0234) and used to  
 CC design primers (736795-808) utilized in the isolation of a cDNA  
 CC clone (736785) coding for PSM. The isolated cDNA and PSM protein  
 CC were used to design primers for the diagnosis and treatment  
 CC of prostate cancer and metastasis.  
 CC  
 XX Sequence 19 AA:  
 S0  
 Query Match 2.7%: Score 19; DB 17; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2,3e-12;  
 Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 656 YAGSPGTYALFPIK 674  
 Db 1 YAGSPGTYALFPIK 19  
 RESULT 41  
 M45408 ID M45408 standard; Peptide: 18 AA.  
 XX M45408:  
 XX 06-JUL-1998 (first entry)  
 DT  
 XX PMSA peptide (aa196-213) peptide 6.  
 XX  
 KW Prostate-specific glandular kallikrein; hK2 protein; human;  
 KW prostate-specific antigen; PSA; hK3; prostate carcinoma;  
 KW prostate cancer; benign prostatic hyperplasia; diagnosis; PMSA.  
 XX  
 OB Synthetic.  
 XX  
 PH Key Location/Qualifiers  
 PT Cleavage-site 9..10  
 PT Cleavage-site 14..15  
 PT Cleavage-site 14..15

R55102 ID R55102 standard; Peptide: 22 AA.  
 XX R55102:  
 XX 11-JAN-1995 (first entry)  
 DT  
 XX Prostate-specific membrane antigen peptide fragment.  
 XX  
 KW Prostate-specific membrane antigen; PSM; prostate cancer;  
 KW transmembrane glycoprotein; imaging; targeting; tumour detection;  
 KW antibody detection; sequencing.  
 XX  
 OB Homo sapiens.  
 XX  
 PH Key Location/Qualifiers  
 PT Miso-difference 4 /note= "unidentified residue"  
 PT Miso-difference 4 /note= "unidentified residue"  
 PT M09409820-A.  
 XX  
 PD 11-MAY-1994.  
 XX  
 XX 05-NOV-1993: 93MO-0510624.  
 XX  
 PR 05-NOV-1993: 93DS-0973337.  
 XX  
 PA (SLOAN ) SLOAN KETTERING INST CANCER.  
 XX  
 XX PAIR NR, Heaton MDM, Israel RS.  
 XX WPI: 1994-16719/20.  
 DR  
 XX Prostate-specific membrane antigen and DNA encoding it - 1st  
 XX PT useful for detecting hematogenous micro-metastatic tumour cells  
 XX PT and for identifying ligands which bind to PSM Ag  
 XX  
 XX Example : Page 46: 196pp: English.  
 CC The inventors attempted to sequence the PSM Ag by modified Edman  
 CC degradation. Peptides (R55098-107) that gave clear dominant peaks  
 CC on HPLC from the digested PSM Ag sample were used. Some of the  
 CC peptides were identified by mass spectrometry. Some of these  
 CC levels and identified with lower confidence. Some of these peptides  
 CC were used to design primers to carry out PCR to identify cDNA clones  
 CC encoding the PSM Ag. R55102 was used to design primers G55377-30.  
 CC A cDNA clone (R55102) was identified as a partial PSM sequence  
 CC encoding the PSM Ag. The PSM Ag was sequenced and the sequence  
 CC by G55377-30. The PSM coding sequence is useful for suppressing or

PT Cleavage-site 13..16  
 PT /note= "hK2 cleavage site"  
 XX  
 XX M09802748-A1.  
 XX  
 XX 22-JAN-1998.  
 XX  
 PF 15-JUL-1997: 97MO-0512322.  
 XX  
 XX 15-JUL-1996: 96DS-0680868.  
 XX  
 PR (HYBR-) HYBRITRCH INC.  
 PA (MAYO-) MAYO FOUNDATION.  
 PI Young CL, Klee GG, Mikolajczyk SD, Saeed M, Tindall DJ.  
 XX Young CLP.  
 DR WPI: 1996-120376/11.  
 XX  
 XX Diagnostic methods using antibodies which bind prostate antigens -  
 XX for cancer for c.g. monitoring treatment or progression of prostate  
 XX cancer  
 XX  
 XX Example 7: Fig 16: 100pp: English.  
 XX  
 XX Peptide 6 represents amino acid residues 196-213 of PMSA.  
 XX Peptides 1-6 (see M45402 and M45404-08) were used as substrates to  
 XX CC the examine amidolytic activity of prostate specific antigen (PSA)  
 XX hK3 (see M45398) and of prostate-specific glandular kallikrein hK2  
 XX (see M45397). All peptides tested hK2 had specificity only for  
 XX CC selected arginines, and PSA primarily for selected tyrosine,  
 XX CC phenylalanine and leucine residues. The invention provides  
 XX CC diagnostic methods using antibodies which bind prostate antigens  
 XX CC and methods for monitoring the treatment or  
 XX CC progression of prostate cancer.  
 XX  
 S0 Sequence 18 AA:  
 Query Match 2.5%: Score 18; DB 19; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2,4e-11;  
 Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 152 CCRGIVIRKGRVPRNKK 169  
 Db 1 CCRGIVIRKGRVPRNKK 18  
 RESULT 42

CC modulating the metastatic ability of prostate tumour cells to grow,  
 CC or for eliminating them. The protein is useful to identify or purify  
 CC ligands of the Ags as substrates for the Ags, for Ab-directed  
 CC imaging and targeting of prostate tumour deposits.  
 XX  
 S0 Sequence 22 AA:  
 Query Match 2.4%: Score 17; DB 15; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 3,1e-10;  
 Matches 17: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 34 TQPHLAGTEQNFGLAK 50  
 Db 6 TQPHLAGTEQNFGLAK 22  
 RESULT 43  
 M02241 ID M02241 standard; Peptide: 22 AA.  
 XX M02241:  
 XX 05-NOV-1996 (first entry)  
 DT  
 XX Prostate-specific membrane antigen peptide 2734 6.  
 XX  
 KW Prostate-specific membrane antigen; PSM; prostate cancer;  
 KW metastasis; therapy; diagnosis.  
 XX  
 OB Homo sapiens.  
 XX  
 PH Key Location/Qualifiers  
 PT Miso-difference 4 /note= "unidentified amino acid"  
 PT Miso-difference 5 /note= "unidentified amino acid"  
 PT M09626272-A1.  
 XX  
 XX 29-AUG-1996.  
 XX  
 PF 23-FEB-1996: 96MO-0502424.  
 XX  
 XX 03-JUN-1995: 95DS-0470735.  
 XX 24-FEB-1995: 95DS-0394157.  
 XX 03-JUN-1995: 95DS-0466381.  
 XX  
 PA (SLOAN ) SLOAN KETTERING INST CANCER RES.  
 XX  
 XX PAIR NR, Heaton MDM, Israel RS;

XX WP1: 1996-402365/40.  
 XX DNA encoding alternatively spliced prostate-specific membrane  
 PT antigen - useful to develop prods. for detecting haematogenous  
 PT micrometastatic tumour cells, or prostate cancer progression  
 XX  
 XX Example 1: Page 49: 284bp; English.  
 XX  
 CC Tryptic peptides (W0237-45) were obtd. from the human prostate-  
 CC specific membrane (PSM) antigen (see also W0234) and used to  
 CC design primers (736795-808) utilized in the isolation of a cDNA  
 CC clone (736785) coding for PSM: primers 1-L (736801-04) are  
 CC based on amino acids 14-19 of peptide 2734 6 (W0234). The  
 CC isolated cDNA and PSM protein are useful in developing methods for  
 CC the diagnosis and treatment of prostate cancer and metastasis.  
 XX  
 XX Sequence 22 AA:  
 50  
 Query Match 2.4%; Score 17; DB 17; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 3 1e-10;  
 Matches 17: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 34 ATPTDGLDPPPPYR 50  
 Db 6 EQPHLAGTEQNDIQLX 22

RESULT 44  
 R55105 standard: Peptide: 15 AA.  
 XX R55105:  
 XX 11-JAN-1995 (first entry)  
 XX  
 XX Prostate-specific membrane antigen peptide fragment.  
 XX Prostate-specific membrane antigen: PSM: prostate cancer;  
 XX transmembrane glycoprotein; Imaging: targeting; tumour detection;  
 XX antibody detection: sequencing.  
 XX  
 XX Homo sapiens.  
 XX  
 XX M03409820-A.  
 XX 11-MAY-1994.  
 XX  
 XX 05-NOV-1993; 93MO-US10624.  
 XX

XX metastasis; therapy; diagnosis.  
 XX  
 XX Homo sapiens.  
 XX  
 XX M03626272-A1.  
 XX  
 XX 29-AUG-1996.  
 XX  
 XX  
 XX 23-FEB-1996; 96MO-US07424.  
 XX  
 XX 02-JUN-1995; 95MO-0410735.  
 XX 24-FEB-1995; 95US-0394152.  
 XX 02-JUN-1995; 95US-0466381.  
 XX  
 XX (SLOK) SLOAN KETTERING INST CANCER RES.  
 XX  
 XX Fair WR, Heaton MDM, Israeli RS;  
 XX MPI: 1996-402365/40.  
 XX  
 XX DNA encoding alternatively applied prostate-specific membrane  
 PT antigen - useful to develop prods. for detecting haematogenous  
 PT micrometastatic tumour cells, or prostate cancer progression  
 XX  
 XX Example 1: Page 49: 284bp; English.  
 XX  
 CC Tryptic peptides (W0237-45) were obtd. from the human prostate-  
 CC specific membrane (PSM) antigen (see also W0234) and used to  
 CC design primers (736795-808) utilized in the isolation of a cDNA  
 CC clone (736785) coding for PSM: primers 1-L (736801-04) are  
 CC based on amino acids 14-19 of peptide 2734 6 (W0234). The  
 CC isolated cDNA and PSM protein are useful in developing methods for  
 CC the diagnosis and treatment of prostate cancer and metastasis.  
 XX  
 XX Sequence 15 AA:  
 50  
 Query Match 2.1%; Score 15; DB 17; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2 6e-08;  
 Matches 15: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 630 ATPTDGLDPPPPYR 644  
 Db 1 ATIDPLSDIPYR 15

RESULT 46  
 Y30346 standard: peptide: 16 AA.  
 XX Y30346:  
 XX Y30346:  
 XX Y30346:

XX 05-NOV-1992; 92US-0973337.  
 XX (SLOK) SLOAN KETTERING INST CANCER.  
 XX Fair WR, Heaton MDM, Israeli RS;  
 XX MPI: 1994-167129/20.  
 XX  
 XX Prostate-specific membrane antigen and DNA encoding it - is  
 PT useful for detecting haematogenous micro-metastatic tumour cells  
 PT and for identifying ligands which bind to PSM Ag  
 XX  
 XX Example 1: Page 44: 196bp; English.  
 XX  
 CC The inventors attempted to sequence the PSM Ag by modified Edman  
 CC degradation. Peptides (45508-107) that gave clear dominant peaks  
 CC were identified. Some of these peptides were present in very low  
 CC levels and identified with lower confidence. Some of these peptides  
 CC were used to design primers to carry out PCR to identify cDNA clones  
 CC encoding the PSM Ag. A clone, 1N-20 was identified as a partial PSM  
 CC Ag cDNA. The PSM Ag was then sequenced by the method described  
 CC by G5520). The PSM coding sequence is useful for suppressing or  
 CC modulating the metastatic ability of prostate tumour cells to grow,  
 CC or for eliminating them. The protein is useful to identify or purify  
 CC ligands which bind to the PSM Ag. This is also useful for Mo-directed  
 CC imaging and targeting of prostate tumour deposits.  
 XX  
 XX Sequence 15 AA:  
 50  
 Query Match 2.1%; Score 15; DB 15; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2 6e-08;  
 Matches 15: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 630 ATPTDGLDPPPPYR 644  
 Db 1 ATIDPLSDIPYR 15

RESULT 45  
 W02243 standard: Peptide: 15 AA.  
 XX W02243:  
 XX W02243:  
 XX 05-NOV-1996 (first entry)  
 XX  
 XX Prostate-specific membrane antigen peptide 2738 1.  
 XX  
 XX Prostate-specific membrane antigen: PSM: prostate cancer;  
 XX

XX 15-NOV-1999 (first entry)  
 XX  
 XX N-terminal sequence of the PSM' protein.  
 XX  
 XX PSM' protein; splice variant; prostate specific membrane antigen;  
 XX cancer marker; prostatic cancer.  
 XX  
 XX Synthetic.  
 XX  
 XX Homo sapiens.  
 XX  
 XX M05943710-A1.  
 XX  
 XX 02-SEP-1999.  
 XX  
 XX 22-FEB-1999; 99MO-US03810.  
 XX  
 XX 26-FEB-1998; 98US-0011220.  
 XX  
 XX (BEC-) BECKMAN COULTER INC.  
 XX  
 XX Grauer LG, Kuus-Renel R, Sokoloff R;  
 XX MPI: 1999-540563/45.  
 XX  
 XX New PSM' protein, splice variant of prostate-specific membrane  
 PT antigen, used as marker for prostatic cancer for diagnosis,  
 PT prognosis and treatment  
 XX  
 XX Claim 22: Page 39: 52bp; English.  
 XX  
 CC The present sequence is derived from the N-terminal of the PSM' protein.  
 CC which identifies the PSM' protein. The present sequence can be used to  
 CC raise monoclonal antibodies. Detection of PSM' in a sample, particularly  
 CC using specific antibodies, is useful for diagnosis of prostate cancer.  
 CC In addition, the present sequence is useful for the development of a  
 CC disease. Antibodies may also be coupled to therapeutic agents, such as  
 CC drugs, toxins, etc., and used to treat prostate cancer.  
 XX  
 XX Sequence 16 AA:  
 50  
 Query Match 2.1%; Score 15; DB 20; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2 7e-08;  
 Matches 15: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 16 ATIDELAMINKFL 30  
 Db 1 ATIDELAMINKFL 15





